

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:12:45 : Search time 101.54 Seconds
(without alignments)
444.770 Million cell updates/sec

Title: US-09-052-089a-2
Perfect score: 2393
Sequence: 1 MPILSLCTICSDFFDHSRDV.....VRIKTVSSASQPKLDFLCQ 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	919	38.4	433	2 T30807	TRAF interacting p
2	221	9.2	506	2 F85016	probable RING zinc
3	204.5	8.3	425	2 T23457	hypothetical prote
4	200.5	8.4	1690	2 T13030	microtubule bindin
5	192.5	8.0	1325	2 T42722	male-enhanced anti
6	191.5	8.0	2139	2 T18296	myosin heavy chain
7	190	7.9	2017	1 A36014	myosin heavy chain
8	190	7.9	2057	2 S61477	myosin II heavy ch
9	186.5	7.8	1156	2 E69444	chromosome segrega
10	186.5	7.8	1940	1 S04090	myosin heavy chain
11	185.5	7.8	1039	2 S18199	myosin heavy chain
12	185.5	7.8	1940	1 A24922	myosin heavy chain
13	185.5	7.8	2116	2 A26655	myosin heavy chain
14	183	7.6	1938	2 A40997	myosin heavy chain
15	182.5	7.6	501	2 A38650	myosin heavy chain
16	181	7.6	1156	2 B70356	chromosome assembl
17	181	7.6	2007	1 B43402	myosin heavy chain
18	180	7.5	1992	1 S02771	myosin heavy chain
19	179.5	7.5	1961	1 A61231	myosin heavy chain
20	179.5	7.5	1976	2 A59252	myosin heavy chain
21	179	7.5	1017	2 PC4035	cell-cycle-depende
22	178.5	7.5	1999	1 S21801	myosin heavy chain
23	178	7.4	1970	2 S67593	transport protein
24	177.5	7.4	1957	2 T38077	hypothetical colle
25	177	7.4	2168	1 T30171	ninein - mouse
26	176.5	7.4	1509	1 A27224	myosin heavy chain
27	176.5	7.4	1827	2 T16270	hypothetical prote
28	176	7.4	389	2 B44972	paramyosin - nemat
29	175.5	7.3	1133	2 T22976	hypothetical prote

30	175	7.3	866	2 S04027	paramyosin - Caeno
31	175	7.3	872	2 T19296	hypothetical prote
32	175	7.3	1177	2 B75150	chromosome segrega
33	175	7.3	1313	2 F96673	hypothetical prote
34	174.5	7.3	3225	2 T52300	giantin - human
35	174.5	7.3	3259	1 A56539	myosin - human
36	174	7.3	676	2 S00084	myosin heavy chain
37	173.5	7.3	1203	2 B55094	chromosomal protei
38	172.5	7.2	1313	2 A48467	myosin heavy chain
39	172.5	7.2	1937	2 T38055	myosin heavy chain
40	171.5	7.2	853	2 T51505	hypothetical prote
41	171.5	7.2	876	2 A23767	myosin heavy chain
42	171.5	7.2	1957	2 A59294	skeletal myosin -
43	171	7.1	1130	2 T34081	hypothetical prote
44	171	7.1	1738	2 T14867	interapfin - slime
45	171	7.1	1964	2 A59282	nonmuscle myosin I

ALIGNMENTS

RESULT 1

T30807
TRAF interacting protein - Fugu rubripes
C:Species: Fugu rubripes
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C:Accession: T30807
R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrana, Y.; Wheller, D.; Bishop, M.; Elgar, EBS Lett. 443, 370-374, 1999
A:Title: Three receptor genes for plasmalogen related growth factors in the genome of
A:Reference number: 220880; MUID:99148833
A:Accession: T30807
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-433 <COT>
A:Cross-references: EMBL:AV010317; MID:e1355235; PID:e1355237; PIDN:CAA09084.1
A:Genetics:
A:Gene: TRIP
A:Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match	38.4%	Score 919;	DB 2;	Length 433;
Best Local Similarity	40.7%;	Pred. No. 1.9e-40;		
Matches 191;	Conservative 87;	Mismatches 117;	Indels 74;	Gaps 6;
QY	1	MPILSLCTICSDFFDHSRDVAHICGTHFLQCLIQMFTAPSRCTPCRCRQVGGKTTIN 60		
DB	1	MPIRAQCTICSDFFDHSRDVAHICGTHFHCCLVRFOTAPRTCCPCRCRQVSTRHIS 60		
QY	61	KLFPDLAQEEENVLDAEFLKNELDVSVAQLSOKDREKDSOAIDTLDLTLEERNATVES 120		
DB	61	RLTFDVGLDSSVGPDPESLQNELDVRKYNFSSKEKDEKRAKADDLMEYELQKALEN 120		
QY	121	LQNLNKAEMLCSTLKQMKFLQRODETQKQAREBAHRLCKMKTMEQIELLOSQSEV 180		
DB	121	LQKDVMEKELCSALRTQMTVLESQHNDTRAKEEVRRLIKMTFFSLDVLQGOAEV 180		
QY	181	EEFMRDQGVGSAYBQVLAVVCYSLAKKEYENLKEARKATGELADRLKRLVSSRSKLTLN 240		
DB	181	ESMTIDMIGAAVQOLSTIYCSILKKEYDNKGGKSSNCEKLRKREVLTSNNKLHVAL 240		
QY	241	TELDQAKLEKSAOKDLOSAODEITSLRKKSDDPGNGLEPPASATVEVSRVFPAPVE 300		
DB	241	LELTARDDKMSLQNDLINAKEKISSLKKYEFLOEALSTPRINEALGRIFFEKCGAP 300		
QY	301	MMNPR-----LHOPFGEIDLNTTFDVNTPPTQSSGSHCLPKKLCLEBARSPQNVL 354		
DB	301	PONSVRKASCLHPPSGNEDIDLNTYDVTTPD-----DVAKRRKQVPS 344		
QY	355	KKVHVKSPEQSLSGGRCVGEIDDELAGAPPLFIRNAVIGOKOPNTTIESRSTIVV 414		
DB	345	KKM-----LDSVV-----ILRTYKKNLVNSQGR---FV 371		

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QY      415 KIGFDGLGRTKFIQPRDTHIRPVVSKAKSKÖKVRIKTIVSSASÖPK 463
          :|:||||||| | | | | |
Db      372 QSGYDGLGRKFIQPTIHVR-----SEASKPE 401
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RESULT      2
F85016
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 16-Feb-2001 #sequence-revision 16-Feb-2001 #text-change 16-Feb-2001
C:Accession: F85016
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: F85016
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <SMO>
A:Cross-references: GB:MC_001268; MID:g7267624; PIDN:CAB80936.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g01270
A:Map position: 4

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Query Match	9.2%	Pred. 221	DB 2	length 506	••
Best Local Similarity	21.9%	Pred. No. 0.00019			
Matches 120; Conservative	79;	Mismatches 193;	Indels 156;	Gaps 24	

OY		5	S L C I G S D --- F P D H R D V A A I I G H T P H O C I O M E F N A P S --- R T C Q C S I O Y G K K T	57
Dd		10	A I C I C T C E D L K P V Y E N I Q S I S A - C G V H F E L C I Q O M F F E Y C P S T N K N R C I Q O K S L K O	67
OY		58	I I N K L F P D L A O E E N V L ----- D A E F L K E L D S V K A O L ---- S O K R E K R D S O A I I	104
Dd		68	P C B L Y P Q S S G N Q D S I A S D K V Y G I E E D P V L L R G V K R L B E C K Y O N L S A L E K K K E N V S	127
OY		105	D T L F D T L E ----- E R N A Y E S I Q N A L N K A E M I C S T L K K O M F L E O R O D E T Y O A R F ,	154
Dd		128	D K L H Q C N E O L K E D K V K R M E A L O E I S T Q H L L K L K S E C I O L N S Q C V L Q E R --- T V A L A K	184
OY		155	E A H R L K C ----- K M K M E O I E L L O S ----- Q R S E V E M I R -- D M G V	189
Dd		185	E L A S L K L V S D L S E E D V Y L K A L L I G N N A K K T D I T L V K S L Y I R N R S Y K F L L K K M O L G R	244
OY		190	G O S - A V E O L A V Y C V L K K E Y E N L K E A R K A G E L A D R L K D L V S S R S K L K L N T E L D O A K L	248
Dd		245	G E A S S E K L E A L E K I E K L K R M E L L I T E E R R N R A L R I N N S K --- K C S Y T E V S E P A I	301
OY		249	E L R S A Q D L O S A D O E I T S L R K K S D D P P G N L E P A S A T N E T V S R L V F E S P A V E M N P R L H O	308
Dd		302	E S M S S F R M L - S S D K V --- E K I S T P G K L E E K D F T I Q S C L ----- R G R E	343
OY		309	P P E F D E L M T T P V N --- T P P O T S --- S O H C L P K L C L E R A R S P M O N V L	354
Dd		344	D S F V S R I D --- S V I D V D D Y P P E T N T S O I R M W N T I E E K G D N S M W K D J K E N I R K D P T S V -	400
OY		355	K V Y H V K S P E S O --- L S L G O R C V G ----- E L D E L A G A F P L I R N A V L G O K O	399
Dd		401	----- S P I S N S G N I W O S S G T N R N R I G R M S K H G E R N E A T P S L G S V P -----	441
OY		400	P N R T T A S R S S T D V Y R I G F D G L G R T K F I O P R D T T I I R P V K S K A S K O --- K V R I	453
Dd		442	----- R K D D L I S I G P G K G G R I K --- V L R S P Q I S K T W A S G S K R P K L G	484
OY		454	K T V S S A S O 461	
Dd		485	K T S G S S S O 492	

RESULT 3
T25457
hypothetical protein B0432.9 - *Caenorhabditis elegans*

C:Species: *Cenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 02-Sep-2000
C:Accession: J25457
R:Henkhaus, J.; Wohlmann, P.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of *C. elegans* cosmid B0432.
A:Reference number: 220038
A:Accession: J25457
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-425 <HEN>
A:Cross-references: EMBL:U08036, PID:ABJ7893.1, GSPDB:GN00020, CESP:B0432.9
A:Experimental source: strain Bristol N2; clone B0432
A:Genetics:
A:Gene: CESP:B0432.9
A:Map position: 2
A:Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2
C:Superfamily: RING finger homology
E:188-238/Domain: RING finger homology <RRN>

Query Match	8.5%	Score 204.5;	DB 2;	Length 425;
Best Local Similarity	25.9%;	Pred. No. 0.0011;		
Matches 73; Conservative	49;	Mismatches 105;	Indels 55;	Gaps 12

Qy	2	PII\$J---CII\$CDEPDH\$RDVAIIHG\$FH\$DLOCI\$WIEFTAP\$SRPC\$OIR\$YOGKTI	58
Db	184	PII\$SI\$GSC\$IC\$IEDK\$KONK\$ISAIVC\$GHIYH\$GIC\$ISOMAT--KROCP\$SRIRVP\$KNGF	2411
Qy	59	INKLEFFDIAQ---EEENVLDAEFL\$KNEBLS\$YKAOL\$OKDREK\$RDSQAIIIDLTRP\$LEERN	115
Db	242	VEKLEFFDVG\$RMG\$EAEK\$PPEIDY\$REEHY-----KLT\$SL\$KAEK\$IG\$TLT\$ENK\$NKD--	294
Qy	116	ATVE\$LOAL-----NKAEML\$C\$TL\$K\$OK\$P\$LEQ\$ODET\$K\$ARE\$AH\$K\$CK\$MT\$B\$IEL	1717
Db	295	-TV\$KLEKKII\$REK\$DK\$KOEI\$PK\$Q\$AT\$TNH\$LT\$IS\$E\$T\$AY\$K\$K\$REL\$O\$SK\$N\$K\$L\$K\$C\$E\$Y\$KI	3535
Qy	172	LLOS\$R\$EVE\$E\$MIR\$DM\$G\$O\$S\$AVE\$D\$A\$V\$Y\$C\$V\$SLK-----EY\$EN\$K\$E\$K\$AR\$K\$AT\$EL\$D\$RL\$K	227
Db	354	LTVH-----S\$EAD\$Q\$OL\$GEY---L\$K\$N\$G\$N\$LD\$T\$E\$K\$F\$Q\$LM\$K\$P-----NK	389
Qy	228	DIV\$SR\$K\$LT\$NL\$T\$N\$EL\$D\$AK\$IEL\$R\$SA\$K\$OD\$O\$S\$AD\$O\$E\$T\$SL\$K	269
Db	390	DLTDR---REAREIEOL\$K\$EVS--LK\$RA\$O\$E\$PA\$AL\$K	424

RESULT 4
T13030
microtubule binding protein D-CLIP-190 - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text-change 17-Nov-2000
C:Accession: T13030
R:Rantze, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A:Title: A class VI unconventional myosin is associated with a homologue of a microtu
A:Reference number: 217588; MUID: 98135549
A:Accession: T13030
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1690 <LAN>
A:Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A:Experimental source: strain Oregon R
C:Genetics:
A:Cross-references: FlyBase:FBgn0020503
C:Keywords: cytoskeleton

```
Query Match      8.4% Score 200.5; DB 2; Length 1690;  
Best Local Similarity    22.7%; Pred. No. 0.0085;  
Matches 109; Conservative   73; Mismatches 168; Indels 131; Gaps 18;
```

OY 50 RIQVKKTIINKLPDIAOEENVIDAETLNKE-----LDSVKAKLSGSKDKREKRDSDAI 103
::: : :: :
::: : :: :

Dh 724 QIOLEKESIDQAL-----KONELE-DFOKROSESEVHLQETKAQNTOKDLELVESGES 777
Qy 104 IDTLRDLTEERNATVESLQNALNKAEMLCSTIKROMK-FLTEORODETKOAREEAPHRKCK 162
Dh 778 LKRIQOOLEEETTLGHEKLOALEE-----LKKEKETITKEKQEOLOQOSKAESESA 830
Qy 163 MKTME-QIELLLOSQSEVEEMIRDMGVGOSAVBOLAVVCSLKEEYENLKEARKATGEL 221
Dh 831 LKVVQVQLEQLOQQAASGEE-----GSKTVAKLHDEISQLKSQALETQSELKSTESN 883
Qy 222 ADRLKRLVSSRSKLK-----TLNTELDQAKIELLSAQKDLOSADQETSLKKSDDP 274
Dh 884 LEAKSOKLEANGSLSEBAKSGOLOEQITIKLSEVEBETOAAALSYHTDVESTKQO---- 939
Qy 275 PGNLEPASNETVSRVLFESPA-----PVEPMANPRLO-----PPF 311
Dh 940 ----LEAMNALEKYNKEAESAASDLQDKVKETITDLHAELQAEKSSSSALHTKLKSF 966
Qy 312 GDEI-----DLNTEFDVNTPTQTSQSHCLPKKLCLERARSPMO----- 351
Dh 997 SDEIATGHKELTSKAD-----AMSQEMLOKKEKELQELRQLODSQDSQTKLKAGER 1048
Qy 352 -----NVLKVKYKVSKEPESQSLSGQRCVGEDELDELAGAPFLFIRNAVVGOKOPN 401
Dh 1049 KEKSFESIKNLOEVRKAKTENLELSTGTQTTIKDLOERLE-----ITNAELQHK--- 1099
Qy 402 RTTASRSSTDVVRIGFDGLGRTKFIQPRD-TTIIRPVYKSKAKSKQVKRITVSAS 460
Dh 1100 -----EKMASEDAKTA-----DLKTLVEAIOVANANISATNAELSTVLEVL 1141
Qy 461 Q 461
Dh 1142 Q 1142

RESULT 5
T42722
male-enhanced antigen-2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_rev1sion 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T42722
R:Kondo, M.; Sutoh, S.
DNA Seq: 7, 71-82, 1997
A:Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhanced
A:Reference number: Z22242; MUID:97217683
A:Accession: T42722
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1325 <KON>
A:Cross-references: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BAAI19612.1
A:Experimental source: strain CD-1
C:Function:
A:Description: supposed to play some role for spermatogenesis
C:Keywords: leucine zipper

Query Match 8.0%; Score 192.5; DB 2; Length 1325;
Best local Similarity 22.4%; Pred. No. 0.017;
Matches 94; Conservative 80; Mismatches 156; Indels 89; Gaps 16;

Qy 65 DLAOEENVLDA-EFLKNE-----LDSYKAOLSQDKREKR-----DSQAIIIDTLRD 109
Dh 590 ELQREADSRDAIHFLQNEKLVLEVALQSAKSDKELDRGARLEEDTEETSGLEQLRQ 649
Qy 110 TLERNATVESLQNALNKAEMLCSTIKQK-----KFLQO-----RQET-----KQ 151
Dh 650 DLAVKSNQVEHLQOE-----TATLRQOKQKVEQOQVQVMEAVARRDATSKDOLINE 702
Qy 152 AREEHNRLCKMKTMEQIETLLQSORSEVE-----EMIRDMGVGOSAVBOLAVVCSLKE 207
Dh 703 LKATKRLDSEMKELRQELIKLOGEKKTVEVHSHLQKDMSLVHQQAELGSHQSOVKE 762
Qy 208 YEN-----LKEA-----RKATGELADRLKDLVSSRSKLKTLNTELDQA 246

Dh 763 RDEMEIHLQSLKFDKEQIMALTAEANETLKQIPELOQEAQKATTEQOKKKRIGSDLTSA 822
Qy 247 KLELSAQKLOLSADQETITSLRKSDDPNGNLBPASTNTVRIEVPAPVEMNPR 306
Dh 823 QKEKKTTHKAYENA-----VSTLSRRLOEA-----LASKRETDDELQOLRAQSTG--GSSDPVL 874
Qy 307 HOPPFGEIDLNTT-----FDVNTPTQTSQSHCLPKKLCLERARSPMOVLKVV 357
Dh 875 HEKIRALEVELQNVGOSKILLEKELOEVITMTQSOELSESEKVELEDELQESRGFRKI 934
Qy 358 HVSKEPESQSLSGQRCVGEDELDELAGAPFLFIRNAVVGOKOPNRTTAESSSTDVRI 416
Dh 935 KRLSESNKLTAL-----ELEHERGKLTGIGOSNALLREHNSILETALAKREADIVOL 986

RESULT 6
T18296
myosin heavy chain - Entamoeba histolytica
C:Species: Entamoeba histolytica
C>Date: 15-Oct-1999 #sequence_rev1sion 15-Oct-1999 #text_change 08-Sep-2000
C:Accession: T18296
R:Guillen, N.
Submitted to the EMBL Data Library, February 1997
A:Reference number: Z18865
A:Accession: T18296
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2139 <GUT>
A:Cross-references: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AA848065.1
C:Genetics:
A:Gene: mhca
A:Superfamily: myosin heavy chain; myosin motor domain homology
F:91-780/Domain: myosin motor domain homology <MMO>

Query Match 8.0%; Score 191.5; DB 2; Length 2139;
Best local Similarity 22.1%; Pred. No. 0.032;
Matches 97; Conservative 83; Mismatches 161; Indels 97; Gaps 16;

Qy 66 LAOEENVLDAEFLKNEQSLQKLSQK-----DREKDSQAIIIDTLADTEERNATV 118
Dh 1671 VAOEERK-----QRLSDIAELKEQLEOERTTANAEEARRKIQAELEDFVFNLEDVTNR 1726
Qy 119 EST--QNALNKAEMLCSTIKKQKMFLEORODETKOAREEAPHRKCKMKTMEQIELLQSO 176
Dh 1727 EKLVAKNSENDAT--DSLKEEKALE---DELEKITDNNKLS-----EEDSLDRKY 1775
Qy 177 RSEVEEMIRDMGVGOSAVEQLAVVCSLKEEYENLKEARKATGELADRLKDLVSSRSKL 236
Dh 1776 NALLDSKSDSVSMKEKQODELKYTKDALFETKKNHAETMLRG-----RLEKEAAEYQVRL 1831
Qy 237 KTLNTELDQAKLELRSQKLOLSADQETITSLRKSDDPNGNLBPASTNTVSRVLFESP 296
Dh 1832 EALQKNLDLAQOEKAKATKQVRAADGELKSLMNLDELVDKQDLDA----- 1876
Qy 297 APVEMANPRLOHPFGEIDLNTFED-----VNTPTQTSQSHCLPKKLCL-----R 345
Dh 1877 -----QDLADDEDLATLQDKYKTLVQKQSVFDSRIQ--MOBQIDLEKAGRAK 1924
Qy 346 ARSPMOVLKVKHVSKEPESQSL-----SLGQRCVGEDELDELAGAPFLFIRNA 393
Dh 1925 AQOKQAYEKKLQLEQENDNDFEYKETAQRKITLSAQK--DDLOQL-----EK 1973
Qy 394 VLQOKOPNRTTAE-----SRSTDVVRIGFDGLGRTKFIQPRDITTIIRPVYKSKAKS 447
Dh 1974 ERGLKQSEKEVQRLRVKCOELFETKVAEYG--GANVSIKAKYKAYEADIEBLTTEADAL 2031
Qy 448 KQYVRITVSSASOPKLD 465
Dh 2032 KAKKAEKKAKTQSOKLD 2049

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RESULT 7
A36014
myosin heavy chain, nonmuscle - fruit fly (Drosophila melanogaster)
N:Contents: myosin ATPase (PDB 3.6.1.32)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: A36014; B36014
R:Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990
A:Title: Complete sequence of the Drosophila nonmuscle myosin heavy-chain transcript: cd
A:Reference number: A36014; MUID:90348606
A:Accession: A36014
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2017 <KET>
A:Cross-references: GB:M35012
A:Genetics:
A:Gene: FlyBase:zfp
A:Cross-references: FlyBase:Fbgn0005634
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated
F:1-2017/Product: myosin heavy chain, form I #status predicted <MA1>
F:4-2017/Product: myosin heavy chain, form II #status predicted <MA2>
F:135-815/Domain: myosin motor domain homology <MMOT>
F:225-232/Region: nucleotide-binding motif A (P-loop)
F:598-631/Region: actin binding #status predicted
F:705-727/Region: actin binding #status predicted
F:888-2017/Domain: coiled coil #status predicted <COI>
F:888-1328/Region: S2
F:1329-2017/Region: light meromyosin
F:176/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F:21/Binding site: ATP (Lys) #status predicted
F:745,755/Active site: Cys #status predicted

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Query Match 7.9%; Score 190; DB 1; Length 2017;
Best Local Similarity 23.8%; Pred. No. 0.036;
Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFFDLQEEENVLDAE--FLKNELDSVKAQLSQKREKRSQ-----AI 103
DB 1263 KTVLEK-----AKGTLEENADLATELSRVSSNQENDRRKQAESQIAELQVKLAE 1314
QY 104 IDTLRDTLEER---NATVESLONALKAEMLCSTLKKOMFLERODETKQAREEAAHR- 158
DB 1315 IERARSELQEKCTKIQOEAENITNQLEAEALKAASAVASNMESQLEAQOQLLEETRPQ 1374
QY 159 ---LKCKMKTMEOJELLQSORSEVEEMIRDMGVSAGAVEQALAVCVSLKKEYENLKEAR 215
DB 1375 KLGLSSKLRQIESKEKALQEOLEEDDEAKRNY---EKRLAEVTTQMOEIKKAEEDADLA 1431
QY 216 KATGELADRLKKDLVSSRSKLTLL--NTELDQAKLELRSAQKD---LQSADEITSRLR 268
DB 1432 KELEBGRKRLKQIDLEALEROVKELIAQNDRLDKSKKKIQSLELDATIELEQRTKVELE 1491
QY 269 KKSDDPPGNLEPASATMETVSRVLFESPAPEVMNPRLHQPPEDEIDLNTFPVNTPTPT 328
DB 1492 KKQK---NPKKILAEKKAISEQIAQERDTAREAREKETKTVLSVSRLEDAFP----- 1541
QY 329 QTSQSQHCLPKKICLERARSPMNVL-----KVVHKVSKP---ESQLS-LGGQ 372
DB 1542 -----KIEDLENKRTKLQNELDLANTQCTADKNVHELKAKRALESQIAELKQ 1591
QY 373 RCVGELDEEL 382
DB 1592 N--BELEDL 1599

```

```

RESULT 8
S61477
myosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Jul-1996 #sequence, revision 26-Jul-1996 #text_change 02-Feb-2001

```

```

C:Accession: S61477; S65349
R:Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
J. Mol. Biol. 255, 98-109, 1996
A:Title: Molecular organization and alternative splicing in zipper, the gene that enc
A:Reference number: S61477; MUID:96144835
A:Accession: S61477
A:Molecule type: DNA
A:Residues: 1-2057 <MAN>
R:Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
submitted to the EMBL Data Library, September 1995
A:Accession: S65349
A:Reference number: S65349
A:Molecule type: DNA
A:Residues: 1-1908 'NL', 1911-2057 <MAN>
A:Cross-references: EMBL:U35816
A:Cross-references: EMBL:U35816; NID:91141789; PIDN:AMB09049.1; PID:91572481
A:Genetics:
A:Gene: zfp
A:Cross-references: FlyBase:Fbgn0005634
A:Intons: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: alternative splicing; ATP; nucleotide binding; P-loop
F:135-855/Domain: myosin motor domain homology <MMOT>
F:225-232/Region: nucleotide-binding motif A (P-loop)

```

```

Query Match 7.9%; Score 190; DB 2; Length 2057;
Best Local Similarity 23.8%; Pred. No. 0.037;
Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14;

QY 56 KTIINKLFFDLQEEENVLDAE--FLKNELDSVKAQLSQKREKRSQ-----AI 103
DB 1303 KTVLEK-----AKGTLEENADLATELSRVSSNQENDRRKQAESQIAELQVKLAE 1354
QY 104 IDTLRDTLEER---NATVESLONALKAEMLCSTLKKOMFLERODETKQAREEAAHR- 158
DB 1355 IERARSELQEKCTKIQOEAENITNQLEAEALKAASAVASNMESQLEAQOQLLEETRPQ 1414
QY 159 ---LKCKMKTMEOJELLQSORSEVEEMIRDMGVSAGAVEQALAVCVSLKKEYENLKEAR 215
DB 1415 KLGLSSKLRQIESKEKALQEOLEEDDEAKRNY---EKRLAEVTTQMOEIKKAEEDADLA 1471
QY 216 KATGELADRLKKDLVSSRSKLTLL--NTELDQAKLELRSAQKD---LQSADEITSRLR 268
DB 1472 KELEBGRKRLKQIDLEALEROVKELIAQNDRLDKSKKKIQSLELDATIELEQRTKVELE 1531
QY 269 KKSDDPPGNLEPASATMETVSRVLFESPAPEVMNPRLHQPPEDEIDLNTFPVNTPTPT 328
DB 1532 KKQK---NPKKILAEKKAISEQIAQERDTAREAREKETKTVLSVSRLEDAFP----- 1581
QY 329 QTSQSQHCLPKKICLERARSPMNVL-----KVVHKVSKP---ESQLS-LGGQ 372
DB 1582 -----KIEDLENKRTKLQNELDLANTQCTADKNVHELKAKRALESQIAELKQ 1631
QY 373 RCVGELDEEL 382
DB 1632 N--BELEDL 1639

```

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RESULT 9
E69444
chromosome segregation protein (smc1) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence, revision 05-Dec-1997 #text_change 02-Jun-2000
C:Accession: E69444
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Arlath, P.; Kaibe, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343

```

A:Accession: E69444
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1156 <LIE>
 A:Cross-references: GB:AE000995; GB:AE000782; NID:g2689318; PIDN:AA89690.1; PID:g264900
 C:Superfamily: chromosome segregation protein SMCI

Query Match 7.8%; Score 186.5; DB 2; Length 1156;
 Best Local Similarity 16.7%; Pred. No. 0.029;
 Matches 78; Conservative 111; Mismatches 152; Indels 125; Gaps 13;

QY 55 KTIINKLFFDLAEEENVL---DAEFLKNE----- 82
 DB 671 KERMLSKIIYELQREKGLFAELNRAESLRQYKDEVDRLTGMISELRNLSLDEKIRI 730
 QY 83 ----LDSVKQQLSKQDKK-----KDSQAIITLDTLEERRATVESLONALNKREML 131
 DB 731 ESGRIEELREKISQSKREKENYISLSDYNSKLAEMEAIGELAEIEIERMLRGE-- 788
 QY 132 CSTLRKQKMFLEQRODETQKQAREAHRLKCKMKT---EQIELLSQ-----RSEV 180
 DB 789 ---VPKIVEELDKKEHQRRRELISIEKKIESLEFKRQLESSEMQEYIYDEIKDRI 845
 QY 181 EEMIRDMGVQSAVEQLAVYCVSLKKEYENLKARKATGELADRLKDLVSSRSKLTN 240
 DB 846 DEIRRTIEEGKARVEEINSELEELRKERELGKLRKREDELKQLRNAEEKKRIE 905
 QY 241 TELDQALELSAOKDQASQDQETSLRKSDDPPGMLRPAATNEVSRIVFESPAPVE 300
 DB 906 AEIDRLERIKLOKERELEISELAEIAGEV--EVPEMLPLEKVEKYLDEVL----- 955
 QY 301 MMNRLHQPPGDEIDNTFEDVNTPTQ-----TSGSQHCLPKCLLERASPMQVNLK 355
 DB 956 -----VELSTGQVNLKAIQEEYEPKARDEIVEKKMLERKRA---DILD 998
 QY 356 KVKVSKPESQSLSGQRCVGEDELAEAGPFLIRNAVLGQKOPNFTTASRSSTDVVR 415
 DB 999 RIEKYEKKREI-----PFEVE-----TAINRFAEIR 1027
 QY 416 IGFGGLGRTKFTIOPRTTIIRPVVSKAKSKVAKIKTVSSASQ 461
 DB 1028 ---ELANGEGELYLDSDPFNSGLYIKVKNPKKPVOKLESMSGCK 1070

RESULT 10
 S04090
 myosin heavy chain 3, skeletal muscle, embryonic - human

N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 19-Jan-2001
 C:Accession: S04090, S06146, S05442, S12460, S09333, A35082
 R:Eller, M.; Steedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Rubinstein, N.A.; Kelly, A.M.
 Nucleic Acids Res. 17, 3591-3592, 1989
 A:Title: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.
 A:Reference number: S04090; MUID:89263803
 A:Accession: S04090
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-1940 <ELI>
 A:Cross-references: EMBL:X13988; NID:g34843; PIDN:CAA32167.1; PID:g34844
 R:Eller, M.; Steedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Wu, O.L.; Raychowdhury, M.K.
 FEBS Lett. 256, 21-28, 1989
 A:Title: Human embryonic myosin heavy chain cDNA. Interspecies sequence conservation of
 A:Reference number: S06146; MUID:90033298
 A:Accession: S06146
 A:Molecule type: mRNA
 A:Residues: 774-1662, 'QT', 1665-1940 <EL2>
 A:Cross-references: EMBL:X13100; NID:g31143; PIDN:CAA31492.1; PID:g31144
 R:Karsch-Mizrachi, I.; Travis, M.; Biau, H.; Leinwand, L.A.
 Nucleic Acids Res. 17, 6167-6179, 1989
 A:Title: Expression and DNA sequence analysis of a human embryonic skeletal muscle myosin
 A:Reference number: S05442; MUID:89366648

A:Accession: S05442
 A:Molecule type: DNA
 A:Residues: 856-1390, 'KK', 1393-1940 <KAR>
 A:Cross-references: EMBL:X15696; NID:g35504; PIDN:CAA33731.1; PID:g1335313
 R:Stedman, H.H.; Eller, M.; Jullian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.
 J. Biol. Chem. 265, 3568-3576, 1990
 A:Title: The human embryonic myosin heavy chain. Complete primary structure reveals e
 A:Reference number: A35082; MUID:90154023
 A:Contents: annotation; chromosomal assignment
 R:Bober, E.
 submitted to the EMBL Data Library, January 1989
 A:Reference number: S12458
 A:Accession: S12458
 A:Molecule type: mRNA
 A:Residues: 856-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>
 A:Cross-references: EMBL:X51593; NID:g29463; PIDN:CAA35942.1; PID:g29464
 R:Experimental source: Clone gCMC-E
 R:Bober, E.; Buchberger-Seldi, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
 Eur. J. Biochem. 189, 55-65, 1990
 A:Title: Identification of three developmentally controlled isoforms of human myosin
 A:Reference number: S09331; MUID:90235862
 A:Accession: S09331

A:Molecule type: mRNA
 A:Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-125
 1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOV>
 A:Cross-references: EMBL:X51593
 C:Genetics:
 A:Gene: GDB:MYH3
 A:Cross-references: GDB:119443; OMIM:160720
 A:Map position: 17p13.1-17p13.1
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; muscle
 F:89-767/Domain: myosin motor domain homology <MOTOR>
 F:179-186/Region: nucleotide-binding motif A (p-loop)
 F:549-586/Region: actin binding status predicted
 F:656-678/Region: actin binding status predicted
 F:840-1940/Domain: coiled coil #status predicted <COI>
 F:840-1280/Region: S2
 F:1281-1940/Region: light meromyosin
 F:130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F:185/Binding site: ATP (Lys) #status predicted
 F:696,706/Active site: Cys #status predicted

Query Match 7.8%; Score 186.5; DB 1; Length 1940;
 Best Local Similarity 20.3%; Pred. No. 0.052;
 Matches 77; Conservative 83; Mismatches 177; Indels 43; Gaps 7;

QY 54 GKTIINKLFFDLAEEENVLDAEFLKNELDVSKAQLSQKREKRSQAIIIDTRDTLE 112
 DB 1262 GKNEIQRSLSELTQKSRLOTEGELSRQLEKESTVLSQSRKQAFQOTETELKQLE 1321
 QY 113 ERNATVESLONALKAMLCSTLKQKFLERODETKQAREAH-----RLCKMKMTM 166
 DB 1322 EENKAKNALAHALQSSRHDCDLREQYEEQEGKAEIQRALSKANSEVAQWRTYETDAI 1381
 QY 167 EQIELLSQSQSEVEEMIRMGVQSAVEQLAVYCVSLK-----EVENLKARKATG 219
 DB 1382 QRTTELEDAQ---EKLAQRLODSEQVEAVNAKCALETKQKORLOQEVDELMDVVERAN 1437
 QY 220 ELADRLKDLVSSRSKKTTLNTELDQAKLELSAQKQDSADQETSLRKSDDPPGNLE 279
 DB 1438 SLAAADLKQKQNFQKVALAEKTKCEQSALEALAKESRSISTFLFKLNAYEALDQLE 1497
 QY 280 PASATNETVSRVLESPAPVEMNPRILHOPFGDEIDLTFTFDVNTPTQTSQSQCPLK 339
 DB 1498 TVKRENNKLEQELIDLTQELAENGKTIHE-----LEKSRKQIDLEK 1538
 QY 340 ---ELCLERARSPQNVNLKVKHKVSKPESQSLSGQRCVGEDELAEAGPFLIRNAVLG 396
 DB 1539 ADIOLALEEAALEHBAKLTQLELVQKSEIDRKIAEKDEIOLKRNQRTV--- 1595
 QY 397 QKOPNRTTASRSSTDVRI 416

Db 1596 ETMOSALDAEVRSRNEAIRL 1615

RESULT 11

myosin heavy chain - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 02-Feb-2001
 C:Accession: S18199
 R:Stewart, A.F.R.; Camoretto-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, S.; Zak, R.
 J. Mol. Evol. 33, 357-366, 1991
 A:Title: Structural and phylogenetic analysis of the chicken ventricular myosin heavy ch
 A:Reference number: S18199; MUID:92130260
 A:Accession: S18199
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1039 <STE>
 A:Cross-references: EMBL:X59552; NID:962995; PIDN:CAA42130.1; PID:962996
 A:Note: in the authors' translation 45-Lys is shown after residue 40, and, consequently,
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP; nucleotide binding; P-loop
 F:402-409/Region: nucleotide-binding motif A (P-loop)

Query Match 7.8%; Score 185.5; DB 2; Length 1039;
 Best Local Similarity 20.2%; Pred. No. 0.029;
 Matches 77; Conservative 82; Mismatches 167; Indels 55; Gaps 10;

59 INKLFPLDLOEENVL--DAEFLKNELDVKAQLSQDKRKRDSQAIDTLRDTLEERNA 116
 Db 369 MTRLMNDLTQTKTKLQSENGEVR-OLEEKESLISQLSRGKTSFTQOIEELRROLEERTK 427
 Oy 117 TVESLONALNKAEMLCSTLKQKMFLEORODETKOAREARLRCKMKMTMEIQLLOSO 176
 Db 428 SKNALHNLQARHDCDLRLQYEEDEPAKALDPAUSKNAEVAQWTKYTDALQTE 487
 Oy 177 RSE--VEEIRDMGVGSAVEQLAVYCVSLKKEYENLK-----EARKATGELADLK 226
 Db 488 ELEDAKKKLLARLOEAEALAEANAKCSLEKAKHRLQNEDEMDMIDLEKANSAAASLDK 547
 Oy 227 KDLYSSRSKLTN--TELDOAKLELRSQAKDQSDQDETSLRKSSDDPPGULEPASA 283
 Db 548 K---QRFQDKIINDMKQKYEESQAELEASQKEARSLSTELFKLNAYEETLDLETLKR 603
 Oy 284 TNETVSRLYFESPAPVEEMNRLHOPPGDEIDLNTTFDVTPPTQTSQSGHCLPKICL 343
 Db 604 ENKMLQEBISDLTMOISEGNKLNH-----ETL-----KVKQVEDEKSEVQAL 647
 Oy 344 ERARSPMONVLKRYKVKSPESQSLSGQRCVGELEDELAGAFPLFIRNAVIGOKOPART 403
 Db 648 EEAGALEHEESKTLRLQLELSQKADPERKLAKEDEMOMI-----RRNOQRT 696
 Oy 404 -----TAESSRSTDVVRI 416
 Db 697 IDSLQSTLDEARSRNEAIRL 717

RESULT 12

myosin heavy chain, skeletal muscle, embryonic - rat
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
 C:Accession: A24922; A23538; B24263
 R:Strehler, E.E.; Strehler-Page, M.A.; Perriard, J.C.; Periasamy, M.; Nadal-Ginard, B.
 J. Mol. Biol. 190, 291-317, 1986
 A:Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy
 A:Reference number: A24922; MUID:87060988
 A:Accession: A24922
 A:Molecule type: DNA
 A:Residues: 1-1940 <STR>
 A:Cross-references: GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PID:g1619328

R:Strehler, E.E.; Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.
 J. Biol. Chem. 260, 468-471, 1985
 A:Title: Intron positions are conserved in the 5' end region of myosin heavy-chain ge
 A:Reference number: A22538; MUID:85080119
 A:Accession: A22538
 A:Molecule type: DNA
 A:Residues: 1-168 <ST2>
 A:Cross-references: GB:L00370; GB:M10135; NID:9205580; PIDN:AAA1655.1; PID:954476
 R:Periasamy, M.; Wydro, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal-Ginard, B.
 J. Biol. Chem. 260, 15856-15862, 1985
 A:Title: Characterization of cDNA and genomic sequences corresponding to an embryonic
 A:Reference number: A24263; MUID:86059474
 A:Accession: B24263
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1358-1490, 'G' <PER>
 A:Cross-references: GB:K03468; NID:g205573; PIDN:AAA1652.1; PID:g205574
 A:Experimental source: clone PMHC-72
 C:Genetics:
 A:Introns: 68/3; 116/3; 169/1
 A:Note: the list of intron positions may be incomplete
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle
 F:89-76/Domain: myosin motor domain homology <MMOT>
 F:179-186/Region: nucleotide-binding motif A (P-loop)
 F:549-586/Region: actin binding #status predicted
 F:656-678/Region: actin binding #status predicted
 F:840-1940/Domain: coiled coil #status predicted <COI>
 F:840-1280/Region: S2
 F:181-1940/Region: light meromyosin
 F:130/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
 F:185/Binding site: ATP (Lys) #status predicted
 F:696,706/Active site: Cys #status predicted

Query Match 7.8%; Score 185.5; DB 1; Length 1940;
 Best Local Similarity 19.5%; Pred. No. 0.059;
 Matches 74; Conservative 84; Mismatches 180; Indels 41; Gaps 7;

54 GKRTIKKLFPLDLOEENVLDAEFLKNELDVKAQLSQDKRKRDSQAIDTLRDTLE 112
 Db 1262 GKNETORSUSELTQTSRLOTENGELSROLEEESIVSLSRSKQAFQOIEELRQLE 1321
 Oy 113 ERNATVESLONALNKAEMLCSTLKQKMFLEORODETKOAREARLRCKMKMTMEIQL 172
 Db 1322 EENAKKALALALOSSRHDCDLRLQYEEDEGAELEQALSKANSEVAQRTYETDAI 1381
 Oy 173 ----LQSRSEVEEMIRDMGVGSAVEQLAVYCVSLK-----EYENLKRAKATGE 220
 Db 1382 QRTLELEAKKILQRLQD--SEQVEAVNAKASLEKTFKORLQGEVEDLMVDVERANS 1438
 Oy 221 LADYLKDDLYSSRSKLTNLTDELDAKLELRSQAKDQSDQDETSLRKSSDDPPGULEP 280
 Db 1439 LAAALDKORNFQVLAEMWKCEESQAELEAALKESRSSTELFKLNAYEETLDLETL 1498
 Oy 281 ASATNETVSRLYFESPAPVEEMNRLHOPPGDEIDLNTTFDVTPPTQTSQSGHCLPK 339
 Db 1499 VKRENKMLQEBISDLTMOISEGNKSIH-----LEKSRKQMELEKA 1539
 Oy 340 --KICLERARSPMONVLKRYKVKSPESQSLSGQRCVGELEDELAGAFPLFIRNAVIGQ 397
 Db 1540 DQWALEEAEALHEBAKILRIQLLETQVSEIDRKIAEKDEIEQLKRYQRTV---E 1596
 Oy 398 KOPKRTTAESRSSSTDVVRI 416
 Db 1597 TMOGALDAEVRSRNEAIRL 1615

RESULT 13

myosin heavy chain [similarity] - slime mold (Dictyostellium discoideum)
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Dictyostellium discoideum

	Query Match	7.6%	Score 182.5:	DB 2:	Length 501:
	Best Local Similarity	22.0%:	Fred. No. 0.018:		
	Matches	76:	Conservative	78:	Mismatches 141: Indels 51: Gaps 9:
Oy	68	OEENEVLDAAEFKLNELDSYKAOLSOKDREKRDSQAIIIDTLRPTLEERNATVESLONALCNK	127		
		: : : : : : : : : : : : : : : :			
Db	30	ONKOQLADMEDLMSSKDDYGKNVHLELSKRALDEOOVEEMRKQLELEDDELQATEDAKIR	89		
Oy	128	AEMLCSTLKQKKFLQRODE-----TKQAREEAHRLLCKMK-----TMEQIEL	171		
		: : : : : : : : : : : : : : : :			
Db	90	LEVNTQAMKAQEPERLOARDEOSEEEKRRLLTGQVRELFEALEDERQRORALAVALSKKMEI	149		
Oy	172	LLOSRSVEEHEIRRMGSGQSAVEDOLAVYCVLKEYEHLKARKATGGLADRLKL DVS	231		
		: : : : : : : : : : : : : : : :			
Db	150	DLKDLEAQIEAANK---ARRRVKQLRRILOAQMKRYQRELEAKRSRDEIFAQSE----	202		
Oy	232	SRSKLTINTTELDOAKLELSAQKDLQSADOETISLRKSDPPGNLEPASTNFTVSR L	291		
		: : : : : : : : : : : : : :			
Db	203	SKKTSLKSLEAEILIQOEELASSERRARRHAQEGRDEL---ADBIANSASGSALLDEKRRL	259		
Oy	292	-----VFESAPVPEMMNPRLHQPPFGDEIDLNTTFEDVNTPTQTSGSQHCLPK--	339		
		: : : : : : : : : : : : : : : :			
Db	260	EARMROLBEELLEEEOSENELLNDLDRFK-----TTIQVDITINAEILAERSAAOKSD	309		
Oy	340	--KLCLEPARSPMNVNLKKVKHKSKRPESQLSG--QRCVGELDEBL	382		
		: : : : : : : : : : : : : :			
Db	310	NAROOLERONDKLAKLOLELGAVSKFRATISSALEAKINGOLEEOL	355		

RESULT 16
B70356
chromosome assembly protein homolog - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
C:Accession: B70356
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: B70356
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1156 <ADP>
A:Cross-references: GB:AE000699; NID:g2983238; PID:g2983243; GB:AE000699
A:Experimental source: strain VFS
C:Genetics:
A:Gene: xcpC
A:Superfamily: chromosome segregation protein SMC1

Query Match	7.6%	Score 181;	DB 2;	Length 1156;
Best Local Similarity	20.1%;	Pred. No. 0.055;		
Matches 81; Conservative	92;	Mismatches 141;	Indels 88;	Gaps 16;

```
OY      66 LAOEENY---LDAEFLKNELDSVKAOLSOKDREKRDQOAIID---TLRDTLEENAVTE   119  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     LKEEREKLEKRELORIKRETBA-KILKEKELLKEERILNELSRESIEDITTFQIO   265  
  
OY      120 SLONAKAEMLCSTLLKKO-----KPLEODETKOAREAHRLCKKKTMEQTEL   171  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     ENEKLNERERLIKLEVENEKIIMPFEKVGTAEIENARSRISIEKERELKESEBNRYNLEE   325  
  
OY      172 LLQSORSVEEMIRMGOGSAVEPOLAYCVSLKFEVENLKEARATGELDRCLKDLS   231  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     LINNLISLKENIERGVGLTOLELEK-----LKEYSLSLEY-----               361  
  
OY      232 SRSKLTINTELDAQKL---ELRSAOKDLQSDAOEITSLRKSDDPGNLBPASATN---   285  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     EREREKRELEEBEEERKAITFDEVKKLEEBEEKETELUNSLNKEQQL--EIQRANIKNIE   419  
  
OY      286 ---ETVSRLVLESBPAY-----EMMNDRLHOPPGDEIDL-NTTFDVNTPPTQTSSQH   335  
| : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  

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Db 420 RIKEDINMLISEREKIKEIKEREQELIKRLAIKKKEEBELRLNTOLENIYEK-----473
QY 336 CLPKKLCLERRASPMONVLLKVKHKVSKPESOLSIGORCAGELDEELAGAPLFLIRNAVL 395S
Db 474 -----LSEYRKKEELKEELKGAIERVRS-----DSDVKRDKRIGVGSV--SELI 519I
QY 396 GOKOPNRTAESSRSTDVYRIGEDLGCRKFIOPRPTTIIR 437
Db 520 RYKNEPHITA-----LEVAG-GGRKFIVEEDEVAK 550

```

RESULT 17
B43402
myosin heavy chain-B, neuronal - chicken
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: B43402; A43402
R:Takahashi, M.; Kawamoto, S.; Adelstein, R. S.
J. Biol. Chem. 267, 17864-17871, 1992
A:Title: Evidence for inserted sequences in the head region of nonmuscle myosin spectrin.
myosin.

A:Reference number: BA3402; MUID:92388144
A:Accession: nb3402
A:Molecule type: mRNA
A:Residues: 1-2007 <RNA>
A:Cross-references: GB:M93676; NID:g212448; PIDN:AAA4988.1; PID:g212452
A>Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide A:Accession: M43402
A:Molecule type: mRNA
A:Residues: 1-211;222-631;653-2007 <TA2>
A:Cross-references: GB:M93676; NID:g212448; PIDN:AAA4988.1; PID:g212449
A>Note: sequence extracted from NCBI backbone (NCBI:n112864)
C:Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyla E:1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>
F:1-211;222-631;653-2007/Product: myosin heavy chain-B, nonmuscle #status predicted <F88-802/Domain: myosin motor domain homology <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)
F:212-221/Region: alternatively spliced segment 1 #status experimental
F:559-593/Region: actin binding #status predicted
F:632-652/Region: alternatively spliced segment 2 #status experimental
F:692-714/Region: actin binding #status predicted
F:875-2007/Domain: coiled coil #status predicted <COI>
F:875-1315/Region: S2
F:1316-2007/Region: light meromyosin
F:129/Modified site: N6;N6-Crimethyllysine (Lys) #status predicted
F:184/Binding site: ATP (Lys) #status predicted
F:732;742/Active site: Cys #status predicted
F:1954/Binding site: phosphate (Thr) (covalent) #status predicted
F:1987/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match	7.68;	Score 181;	DB 1;	Length 2007;
Best Local Similarity	21.58;	Pred. No. 0.1;		
Matches 96;	Conservative 87;	Mismatches 167;	Indels 96;	Gaps 16

Qy	68	QEEENVNDAEFLKRLKELDSVYAAQLSOKNDRKREDSQALITDPLROTLEBRNNTVESLONALNK	127
Db	1536	QNKOTRADMEDELMSKSDYVKNNEHELEKSR-----TLEQOVEEMPTQLEBELDELOA	1586
Qy	128	AEMCSTFLTKOMKLEORODETQOAREPEARLRCMK--KTMEQIELLSQSRSE-----	179
Db	1569	TEDAKLLEVNMAQMKQAFERDIDQARDBQNEEKKRRLVYQVRELEBELEDEKQKQALAVA	1648
Qy	180	----VEEMIRDMGVQ-----SAVEQLAVYCVSLKKEYENLKEARKATGELADRLK	226
Db	1649	AKKKEMDMDL--EQGLEANKARDEATIKQLRLQIQOMQDYQRELEEARASDELPAQSK	1707
Qy	227	KDLVSSSKSLKTLTLELDOAKKLELRSAQCDLOSADDEITSLLKKSDDPGNLLEPASAINE	286
Db	1708	E-----SKRTKLGLEAETILQJQEEFPAASERRRRRAEDOREL---ADELANSASGKSALLD	1760

QY 287 TVSRL-----VFESPAPVEMNPRLLHOPPGDEIDLNTTPTPTPTSGSOHC 336
 Db 1761 EKRLERARIALQLEELQESNMELNFRK-----TTLQVTLNSELAGESSA 1810
 QY 337 LPKKLCLERARSPQWNLKRVH-KVSKPESQLSIGGRCVGEDELDELACGAPFLIRNAV 395
 Db 1811 AOKS---ENAHQOLERQKELKAKLQLEGSVSKFKATISTLEAKINQL-----1857
 QY 396 GOKPKNRTASRSSTDVYRIGFDGLGRTK-----FIQPRD-----TTIIRPVVSKA 445
 Db 1858 -EDELQELAKERRAANKLVR-----RTEKLEKVMQVEDERRHADQYKEQMEKANA 1908
 QY 446 KSKOKVR-----IKTVSSASOPKL 464
 Db 1909 RMKOLKROLEAEERATRANASRRKL 1934

RESULT 18

502771
 myosin heavy chain A [similarity] - Caenorhabditis elegans
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Caenorhabditis elegans
 C>Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
 C:Accession: T23622; S02771
 R:Haris, B.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19773
 A:Accession: T23622
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1992 <NLT>
 A:Cross-references: EMBL:Z78199; PIDN:CA801576.1; GSPDB:GN00023; CESP:K12F2.1
 R:Diib, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
 J. Mol. Biol. 205, 603-613, 1989
 A:Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene
 A:Reference number: S02771; MUID:89178677
 A:Accession: S02771
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-116,140-1992 <DIB>
 A:Cross-references: EMBL:X08067; NID:96798; PIDN:CAA30856.1; PID:96799
 C:Genetics:
 A:Gene: myo-3; CESP:K12F2.1
 A:Map position: 5
 A:Introns: 46/1; 192/1; 292/1; 468/2; 1921/3
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle cc
 F:89-802/Domain: myosin motor domain homology <MMOT>
 F:202-209/Region: nucleotide-binding motif A (P-loop)
 F:680-712/Region: actin binding #status predicted
 F:793-807/Region: actin binding #status predicted
 F:875-1189/Domain: coiled coil #status predicted <COI>
 F:875-1189/Region: S2
 F:1190-1992/Region: light meromyosin
 F:153/Modified site: N6, N6, N6-trimethyllysine (Lys) #status predicted
 F:208/Binding site: ATP (Lys) #status predicted
 F:730,740/Active site: Cys #status predicted

Query Match 7.5%; Score 180; DB 1; Length 1992;
 Best Local Similarity 21.2%; Pred. No. 0.12; Indels 180; Gaps 24;

Matches 126; Conservative 85; Mismatches 203;
 QY 31 LQCLQWETAPSRTPCQRIQVGGKTIINKLPDLQAEENVLDAPFLKNEKLSVKAQL 90
 Db 895 LLEAVQGEIARSOLESQVADLVEEK---NALFLSTETKANKLADAEERNEKLNQKATL 951
 QY 91 SOK-----DREKRSQALIDP-----LRPTLEE---RNTATV 118
 Db 952 ESKSLDITGLEDQEDWERNEDLAROKKKTDOELSDPKKHVQDLESLARRAEDEKOSRDHNI 1011

QY 119 ESLQNALNKAEMLCSTLKQKQKFLQRODETQKQAREAHRLKCKMKTMEQIELLQSOHS 178
 Db 1012 RSLQDEMANQDEAVAKLNKEK---HQEESNRKLNEDLQSEDEKVNHLKIRNKLQEQMD 1068
 QY 179 EVEEMI-----RDMGVGSAVEQULAVYC---VSLKREYENL-----211
 Db 1069 ELEENIDREKRSRGDIKAKKRVGQDLKVAQENIDEITKQKHVDVETTLKREEDLHHTNA 1128
 QY 212 -----KAKKATGELADRLKKDLVS-----SSS-----KKTILNTELDQ 245
 Db 1129 KLAENNSIIAKLQRLIKELTARNALEELAEERSRQKSDRSREARELEELTEERLEQ 1188
 QY 246 -----AKEL-----RSAQKQDSADQDEITSLKKSDDPGNLEPASATNET 287
 Db 1189 QCGATNQLQLEANKKREAIATLRKEKEDSLNHETATISLKKRHODSAVEL---TEQLET 1245
 QY 288 VSRLVFESPAPVEMNPRLLHOPPGDEIDLNT-----TFDVNPPPTTSGSOH-- 335
 Db 1246 LQKLAKSEAKSKLQRLQESSQAHATDSEVRSRQDLKALKTIEVQYSELQTKADEQSRQ 1305
 QY 336 -----CLPKKL-----CLERARSPQWNLKRVH-KVSKPESQLSIGGRCVGEDELDEF-- 381
 Db 1306 LQDFVALKNNRNNNSDNLRLSEEMDNQLSLHRLKSTLQSLQSL-----DETRNNYDEESRE 1361
 QY 382 ---LAGAPFLPFIIRNAVIGOKQPNRTTAESSSTPDVVR-----IGFDGLG-- 422
 Db 1362 RQALAAATKAKNLEHENTILRE---HLDEEASKADLTQISKLNAEIQOKKARPDSELN 1417
 QY 423 -----GRTKFIQPR-----DTTIIRPVVSKAKSKQKVRKIKTVSSASQPKLD 465
 Db 1418 KLEETEAARKALQKLVQELTDTN-----EGLPAKTASQGVKVFRLMQDLDQAQSD 1467

RESULT 19

A61231
 myosin heavy chain nonmuscle form A - human
 N:Alternate names: cellular myosin heavy chain; myosin type 9; NMHC-A
 N:Contains: myosin ATPase (EC 3.6.1.32)
 C:Species: Homo sapiens (man)
 C>Date: 12-May-1994 #sequence_revision 14-Jul-1994 #text_change 19-Jan-2001
 C:Accession: A61231; A34876; 152562; 161692
 R:Simons, M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, C.; Res. 69, 530-539, 1991
 A:Title: Human nonmuscle myosin heavy chains are encoded by two genes located on diff
 A:Reference number: A61231; MUID:91316803
 A:Accession: A61231
 A:Molecule type: mRNA
 A:Residues: 1-715 <SIM>
 A:Cross-references: GB:M69180; NID:g189029; PIDN:AAA61765.1; PID:g189030
 R:Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990
 A:Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through alt
 A:Reference number: A34876; MUID:90138958
 A:Accession: A34876
 A:Molecule type: mRNA
 A:Residues: 715-1961 <SAE>
 A:Cross-references: GB:M1013; NID:g189035; PIDN:AAA36349.1; PID:g189036
 R:Tootaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.
 Blood 78, 1826-1833, 1991
 A:Title: Cellular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones
 A:Reference number: 152562; MUID:92003925
 A:Accession: 152562
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-52, 'EAT', 56-659, 'T', 661-868, 'T', 870-930, 'C', 932-1239, 'KG', 1242-1337 <RE
 A:Cross-references: GB:M8105; NID:g18988; PIDN:AAA5988.1; PID:g553596
 R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
 A:Title: Identification and overlapping expression of multiple unconventional myosin
 A:Reference number: A55758; MUID:94294418
 A:Accession: 161692
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 182-218 <BEM>
A:Cross-references: GB:I29141; NID:9457249; PIDN:AAA20904.1; PID:9531134
C:Genetics:
A:Gene: GDB:MYH9
A:Cross-references: GDB:120216; OMIM:160775
A:Map position: 22q12.3-22q13.1
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleotide
F:84-764/Domain: myosin motor domain homology <MMOT>
F:174-181/Region: nucleotide-binding motif A (P-loop)
F:552-565/Region: actin binding #status predicted
F:837-1938/Domain: coiled coil #status predicted <COI>
F:837-1277/Domain: S2 #status predicted <DS2>
F:1378-1961/Domain: light meromyosin #status predicted <LMW>
F:1939-1961/Domain: carboxyl-terminal <CBT>
F:125/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:180/Binding site: ATP (Lys) #status predicted
F:694/704/Active site: Cys #status predicted

Query Match 7.5% Score 179.5; DB 1; Length 1961;
Best Local Similarity 19.2%; Pred. No. 0.12; Indels 161; Gaps 21;
Matches 108; Conservative 113; Mismatches 181;

QY 48 QCRIOGKRTIINKLFPDLQEEENV-----LDAEF--LKNELDSVKAQLSQK 93
DB 1073 ELKQGLAKKE--EELQALALAVEEAQKNMALKIRLEQISLEQLDSESRNRKA 1130
QY 94 DREKRDGSAIIDTLRLDLEERNATVESIQNALNKAEMLCSTLKK-----QNKLEEQ 144
DB 1131 EKQRDLGEELFAKTELEDTLDSAAQELSRKQEVNLIKLTLEEARHTHEAQIDEM 1190
QY 145 RQ-----DETQKAREARLKKCM-----KTME-----QIELLQSQ-----QREEV 180
DB 1191 RQKISQAVEELAELEQLEQKRAKAMLEKAKQTLNERGELANEVAVLLQGGDSEHKRRKV 1250
QY 181 EEMIRDMGV-----GOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSRSKL 236
DB 1251 EAQQLQELQVKNRGEGRVATLADKVTKQLQVELDVTGLQSSDSKSSKLTGDFALSESQ 1310
QY 237 K-----TLNTELDQAKLELRSAQKDLQSAQDQ-----ITSL 267
DB 1311 QDTQELQLEENRQKLSLSTKLQVEDEKNSFREQLSEEEBAKHNLEKQIATLHAQVADM 1370
QY 268 RKKSDDPGNLEPASATN-----EYKSLVFPSPA---PVEMMNPRLHQPPGDEIDL 317
DB 1371 KKKMEDSVGCLETAEVKKRKLQKDLGLSQHNEEKVAAYDKLTKTRLQOELDDLVDL 1430
QY 318 N-----TTEDVNTPTQTSQSH-----CL 337
DB 1431 DHQKQACNLEKKQKQKFFQDLAEETISAKYAEERDRAEAAREKETKALSLARALEAM 1490
QY 338 PKKICLERAA-----RSPQNVL-----KKYHKVSKPESQSLSGQRC---VGLDEDELA 383
DB 1491 EQKLELRLNKOFTMEDMLSSKDVGVKSVHELEKSRALQEQVEEMKKTQLELEDELQ 1550
QY 384 GAFLEFLTNVAVIGQKOPRTTAESSRSNDVVRIGFDGLGRTKTFLOPRTTIIPV--PVK 442
DB 1551 ATEPAKRLVY-----NLQMKKQAFERD-----LQGDDEQSEKKKQVLQVQVREME 1596
QY 443 SKAKSKQKVRITKTVSSASQPLD 465
DB 1597 AELEDERKQRMVAARAKKLEMD 1619

RESULT 20
A59252
myosin heavy chain, nonmuscle, form IIB - human
N:Alternate names: myosin type 10; NMHC-B
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 02-Feb-2001

C:Accession: A59252; B61231; G02055
R:Phillips, C.L.; Yamakawa, K.; Adelstein, R.S.
J. Muscle Res. Cell. Motil. 16, 379-389, 1995
A:Title: Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and analysis
A:Reference number: A59252; MUID:96023307
A:Accession: A59252
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1976 <SIM>
A:Cross-references: GB:669181; NID:g641957; PIDN:AAA99177.1; PID:g641958
A:Experimental source: clone 11b Lambda Zap II adult human T-cell library; cell line
A:Note: Between nucleotides 1942-1943 in mRNA encoding human brain MHC-B there is an
Circ. Res. 69, 530-539, 1991
A:Title: Human nonmuscle myosin heavy chains are encoded by two genes located on diff
A:Reference number: A61231; MUID:91316803
A:Accession: B61231
A:Molecule type: mRNA
A:Residues: 63-237, 'K', 239-664, 'L', 666-722 <SI2>
A:Cross-references: GB:M69181; NID:g641957
R:Wet, L.
submitted to the EMBL Data Library, August 1995
A:Reference number: H00753
A:Accession: G02055
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-81 <MEI>
A:Cross-references: EMBL:U034304; NID:g1143217; PIDN:AAA84880.1; PID:g1143218
C:Genetics:
A:Gene: GDB:MYH10
A:Cross-references: GDB:127350; GDB:G00-127-350; OMIM:160776
A:Map position: 17p13-17p13
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleo
F:88-771/Domain: myosin motor domain homology <MMOT>
F:118-185/Region: nucleotide-binding motif A (P-loop)
F:559-572/Region: actin binding #status predicted
F:633-647/Region: actin binding #status predicted
F:129/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
F:184/Binding site: ATP (Lys) #status predicted
F:701/711/Active site: Cys #status predicted

Query Match 7.5% Score 179.5; DB 2; Length 1976;
Best Local Similarity 21.8%; Pred. No. 0.12;
Matches 76; Conservative 77; Mismatches 140; Indels 55; Gaps 10;

QY 68 QEEENVDAEFLKNELDVSKAQLSQKDRKDSQAIIIDTLRLDLEERNATVESIQNALNK 127
DB 1505 QNKQLRADMEDMLSSKDVGVKNVHELEKSRALQEQVEEMPTQLELEDELQATEDAKLR 1564
QY 128 AEMLCSTLKKQMKRLQDROD-----TKQAREEARLKKCM-----TMEQIEL 171
DB 1565 LEVNMQAKKQFERDQITRDQNEKKRLLIKQVRELEAELEDERKORALAVASKKMEI 1624
QY 172 LQOSQSEVE--EMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDL 229
DB 1625 DLKQLEAQIEAKNARD-----EVIKQLRKQAQMKQYQRELEEARARSQEIFQSQSE-- 1677
QY 230 VSSRSKTLNTELDQAKLELRSAQKDLQSAQDQITSLRKSSDDPGNLEPASATNFTVS 289
DB 1678 --SEKKLKSLEAETLQLEELASSERARRHAEQDRDEL---ADEITNSASGKSLDDEKR 1732
QY 290 RL-----VESPAPVEMNPRLHQPPGDEIDLNTFTPVNTPTQTSQSGHQLPK 339
DB 1733 RLARIAQLEEELEESQNNMELNDRRK-----TTLQVDTLNAELAEARSAOK 1782
QY 340 ----KLCLERASPMQNVLLKVKHVSKEPSQSLSG--QRCVGLDEEL 382
DB 1783 SDNARQOLEKQNKELKAKLOLEBQAVKSKRATISALEAKIGOLEED 1830

RESULT 21

PC4035
cell-cycle-dependent 350k nuclear protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: PC4035
C:Title: Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.
Biochem. Biophys. Res. Commun. 212, 220-228, 1995
A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for cell cycle regulation
A:Reference number: PC4035; MUID:95336446
A:Accession: PC4035
A:Molecule type: DNA
A:Residues: 1-1017 <LIQ>
A:Cross-references: GB:U5725; NID:9818866; PID:AAA86889.1; PID:9818867
A:Note: Repeat 15-160 and 200-340
C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-term
C:Keywords: nucleoprotein; phosphoprotein
F:45/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #stat
F:85/856/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #statu
F:908/909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pr

Query Match 7.5%; Score 179; DB 2; Length 1017;
Best Local Similarity 21.6%; Pred. No. 0.061;
Matches 86; Conservative 69; Mismatches 159; Indels 84; Gaps 9;
OY 56 KTIINKLFPDLAEEEN---VLDAEFLKNEIDSVKQALQSKDRKRSQAIIIDFLRDTL 111
DB 56 KDKVENLERELQMSFENQELVILDENSKAEEYETLKTQIEEMANSKLVFELDLVTLRSEK 115
OY 112 EERNATVESLONALNKAEMLCSTLKKQMKFLEORQ----- 146
DB 116 ENLFTQIOEGKQGLSELDKLLSPKSGLEKEQAEIQIKESKTAVMELQNLKELNEAV 175
OY 147 -----DEYQAREBAHRLCKAKMTMEQITLLQSQSE----- 179
DB 176 AALCGDOEIMKATEQSIDPPIEEHQILRNISIEKLARLEAEKKQCLVLOQLKESEHNAD 235
OY 180 -----VEEMIRDMGVGQSAVBOAVYCVSLKKEYENLEKARKATGELDRLLKDDVSSRS 234
DB 236 LLKGVNLELERLEIARINOEHMALEANSKGEVETLAKAKTGEMTQSLRGLELDVVTTRS 295
OY 235 KIKTLNTELDQ---AKLET--RSAQKDLQADQETSLRKRSDPPGNT----- 278
DB 296 EKEDLTNELQKEQERISELEIINSFENILOKEQEKVOMKEKSTAMEMLOTQKSSMR 355
OY 279 --EPASATNEYSLVFSPPAVEMNRLHPFG-DEIDIN---TFPDVNTPTQTSG 332
DB 356 EMQPCIMTKKPYSAKEQMLSSQVECLELEKQALQLOGDEAKNNYIVLOSSVNGLIQVEED 415
OY 333 SOHCLPKK-LCLERARSPQWNLKRVHVSKEPESQSL 369
DB 416 GKQKLEKKDEISRLKNOIQDOELVSKLSQVEGEHQL 453

RESULT 22
S21801
myosin heavy chain, neuronal [similarity] - rat
N:Alternate names: myosin II
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: S21801; PNO013; S18134
R:Sun, W.; Chantler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A:Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian brain
A:Reference number: S21801; MUID:92235856
A:Accession: S21801
A:Molecule type: mRNA
A:Residues: 1-1999 <SUN>
A:Cross-references: EMBL:X62659
R:Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A:Title: A unique cellular myosin II exhibiting differential expression in the cerebral

A:Reference number: PNO013; MUID:91151356
A:Accession: PNO013
A:Molecule type: mRNA
A:Residues: 1914-1998, 'I' <SU2>
A:Experimental source: Brain
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; nucleo
F:84/763/Domain: myosin motor domain homology <M003>
F:1174-181/Region: nucleotide-binding motif A (P-loop)
F:541-575/Region: actin binding #status predicted
F:653-675/Region: actin binding #status predicted
F:836-1999/Domain: coiled coil #status predicted <CO1>
F:836-1276/Region: S2
F:1277-1999/Region: light meromyosin
F:125/Modified site: N6/N6, N6-trimethyllysine (Lys) #status predicted
F:180/Binding site: ATP (Lys) #status predicted
F:693/703/Active site: Cys #status predicted
F:1916/Binding site: phosphate (Ser) (covalent) #status predicted
F:1943/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.5%; Score 178.5; DB 1; Length 1999;
Best Local Similarity 20.9%; Pred. No. 0.14;
Matches 93; Conservative 81; Mismatches 153; Indels 117; Gaps 15;
OY 48 QCRIOVGKTIINKLFPDLAEEENV-----LDMEF--LKNELDSVKAQLSQK 93
DB 1072 ELKMOALRKE--EELQALARVEEPAQKNNALKKIRELESQISELDLSESRASRNKA 1129
OY 94 DREKRSQAIIDTLRDLTEERNATVESLONALNKAEMLCSTLKK-----QMKFLEQ 144
DB 1130 EKQKNDLGELEELALKTELEDLDTSTAAQQLRSKKEQEVNLIKLEBEAKTHAQIEM 1189
OY 145 RODETKQAREBAHRL--CKAKMTME-----QIELLOS-----QNSEV 180
DB 1190 ROKHQAEEELAEQLEQTKRVANLEKAKQTLENERGELANEVYKVLQGRDSEKRRKV 1249
OY 181 EEMTDMGV-----GQSAVEQALAVYCVSLKKEYENLEKARKATGELADRLKDDVSSRKL 236
DB 1250 EAQLOELQVKNEGERRVTELDKQTKLQVELDNVTGLISQDSKSKLTDFSALESOL 1309
OY 237 K-----TLNTELDQAKLELSAQKDLQASQDQ-----ITSL 267
DB 1310 QDTQELQLENNQKSLSTFKLQVDEKNSFREQLSEEEEEKHNLKQIATLHQAQVDM 1369
OY 268 RKKSDDPPGNTLEPASATN-----ETVSRLVFESPA---PYEMNPRLLHPPFGEIDL 317
DB 1370 KKKMEDSVGCELTAEVRRKLOKDEGLSORHEEKVAAVADKLEKTRLOQELDLDLVDL 1429
OY 318 N-----TFPDVNTPTQTSGSOHCLPKKLCLEARRSPQWNLKRVHVSKEP 364
DB 1430 DHQROSAONLEKKQKFD-----QLAEETTKSAKYAEERRARDAEERAKATKELSLAR 1483
OY 365 SQLSLGQRC-----VGELDEEL 382
DB 1484 AELFAMEQKAEFLRKNLQEMTERL 1507

RESULT 23
S67593
transport protein USO1 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2552; protein YD058w
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
C:Accession: S67593; A38455; S30782
R:Blocker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67593
A:Molecule type: DNA
A:Residues: 1-1790 <BIO>
A:Cross-references: EMBL:Z74106; NID:91431058; PID:e253003; PID:91431059; MIPS:YDL058
A:Experimental source: strain S288C

R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.
 J. Cell Biol. 113, 245-260, 1991
 A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp
 A:Reference number: A38455; MUID:91185402
 A:Accession: A38455
 A:Molecule type: DNA
 A:Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NAK>
 A:Cross-references: GB:X54378; NID:94777; PIDN:CA948253.1; PID:94778
 A:Note: the authors translated the codon ACT for residue 768 as Ile
 R:Hostetter, M.K.; Herman, D.J.; Bendall, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.
 submitted to the EMBL Data Library, February 1993
 A:Description: An integrin analogue in Saccharomyces cerevisiae.
 A:Reference number: S30782
 A:Accession: S30782
 A:Molecule type: DNA
 A:Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 1462-1580, 'S
 A:Cross-references: EMBL:L03188
 C:Genetics:
 A:Gene: SGD:USO1; INT1
 A:Cross-references: SGD:S0002216; MIPS:YDL058w
 A:Map position: 4L
 C:Keywords: coiled coil; transmembrane protein
 F:326-342/Domain: transmembrane #status predicted <TM1>
 F:394-410/Domain: transmembrane #status predicted <TM2>
 F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match 7.4%; Score 178; DB 2; Length 1790;

Best Local Similarity 18.1%; Pred. No. 0.13; Mismatches 177; Indels 80; Gaps 13;

Matches 81; Conservative 110; Mismatches 177; Indels 80; Gaps 13;

QY 56 KTIINKLFEDLAQEEENVLDA-EFLKNE---LDSVKAQLSOKREKRQSAIIDTLRDT 110
 Db 965 KSLANN-YKDMQAEHESILKAVEESKNESISQLSNLQNKIDSMQEKENFQERSIEKN 1023
 QY 111 LEERATVESIQNA---LNRAEMLCSTLKQMKFLERODETKQAREE-AHRLCKMKMT 165
 Db 1024 IEQLKRTISDLEQTEETISKSDSSKDEESQISLKEKLEFATYANDEENVAKISLTKT 1083
 QY 166 MEOIFELLLOSOREVEEMIRDMVGQSAVEOLAVYCVSLKKRYEMKFKRATGELDR 225
 Db 1084 REELAEELAAKYKLNKNELETKIETSEKAKE-----VKNEEHLEKELQLEKEATET 1136
 QY 226 KDIVVSSRSKLTTLTTELDOAKLELRSQK-----DLQSADEITSL 267
 Db 1137 KOOLNLRANLESLKEHEHDLAQLKRYEEQANKERQYNEEISQLNDEITSTQGENESI 1196
 QY 268 RKSSDPPGNLEPASATMETVSRVLFESPAPEVMNPNRLHQPFEGDEIDLNTFDVNTPP 327
 Db 1197 KKKNDLGEVYKAMKSTSEQSNL---KKSEIDLALNLIKE----- 1234
 QY 328 TQTSQSHCLPRLKLCLEFAR--SPMQNVLKVKYKSPESQSLSGORCVGELDEELAGA 385
 Db 1235 -----LKKNETNDAISLLESTKSYSEVYKIKELODECNF-KEKEVSELEKLAAS 1284
 QY 386 PPLFRNAVIGOKQPNRTTAESRSSTDVVRIGFDGLGRTFTIOPRDYTIIRPVVSK- 444
 Db 1285 EDKNSKYLEL-QKESEKIKEELDAKTTELKQITNLSKAKKESSESLRKTKTSSE 1343
 QY 445 -----AKSKQVRYITVSSASQPKL 464
 Db 1344 RKNAEEOLEKLNETIQKNAQFEKERKL 1371

RESULT 24

T38077
 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38077
 R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: 221767

A:Accession: T38077
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1957 <CON>
 A:Cross-references: EMBL:Z70690; PIDN:CA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
 A:Experimental source: strain 972h-; cosmid c1F3
 C:Genetics:
 A:Gene: SPDB:SPAC1F3.06c
 A:Map position: 1

Query Match 7.4%; Score 177.5; DB 2; Length 1957;

Best Local Similarity 20.6%; Pred. No. 0.15;

Matches 74; Conservative 70; Mismatches 135; Indels 81; Gaps 9;

QY 70 EENVDAEFKNEKLDVYKAQLSOKREKRQSAIIDTLRDLTEERNATVESIQNLNKA 129
 Db 1386 EDNQLATNKLKLDHLOEHLKEDVLEKESLITLSEESLSNOROKESSLDAKNELE 1445
 QY 130 -MLCSTLKQMKFLERQ-----DETQAREEAHRLCKMKMTQETELLOSOREVE 181
 Db 1446 HMLDTSRKNSSLMKESINSISLDDKSFELASAVKELGALQKHSLSLMEINIKSOLQ 1505
 QY 182 EMIRDMVGQSAVEOLAVYCVSLKRYEN-----LKEARKATG 219
 Db 1506 EAKERIQVDESTIOELDHEITASKNNYEGKLNDKDSIIRDSLENIEQLNMLAEKSAVK 1565
 QY 220 ELADLKKDIVSSRSKLTTL-----NPELDOAKLELRSQKIDQASADEITSLRKSD 272
 Db 1566 RISTEKESLIQFNRLADLEYHNKSQVSELSRSLKLAISTTEELQLENEKSLTTTML 1625
 QY 273 DPPGNLEPASATMETVSRVLFESPAPEVMNPNRLHQPFEGDEIDLNTFDVNTPTQSG 332
 Db 1626 DLQNVKQLSNIKDLSE-----DLRTLRSL-DSVASL 1658
 QY 333 SOHCLPKRLCLERARSPMQNVLKVKH-----KVSPPESQSLSGORCVGELDEELAG 384
 Db 1659 QKECKIKSNFVE---SLQDVLTYSQVARNAELEDEVSRSDVKKIRRRDR- EHLHG 1709

RESULT 25

T30171

ninein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T30171

R:Bouckson-Castaigne, V.; Moudjou, M.; Ferguson, D.J.P.; Mucklow, M.; Belkaid, Y.; M1

J. Cell Sci. 109, 179-190, 1996

A:Title: Molecular characterisation of ninein, a new coiled-coil protein of the centr

A:Reference number: 220751; MUID:96431720

A:Accession: T30171

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2168 <BOU>

A:Cross-references: EMBL:U40342; NID:9113864; PID:9113865; PIDN:AAA83234.1

A:Experimental source: Strain C57BL/6

A:Note: localised specifically in the pericentriolar matrix of the centrosome

Query Match 7.4%; Score 177; DB 2; Length 2168;

Best Local Similarity 21.3%; Pred. No. 0.18;

Matches 105; Conservative 83; Mismatches 174; Indels 130; Gaps 21;

QY 31 LQCLQWETAPSRPCQRIQVGGKTIINKLFPDLAQEEENVLDAEFLK-NELDSV--- 86
 Db 1515 LKAMWQ-----PAVTCGEMQ-----RKVELLRESEKLOEENSILKNETITTLNEEDSISNL 1565
 QY 87 -----KAQLSOK-----DREKRQSAIIDTLR---DLTEERNATVE-----SIGNAL 125
 Db 1566 KLEELNGSQBELMKIETIIRBQKASIQTMVEKIKQVSDLIKQQLDSENLSELSQKNSQ 1625
 QY 126 NK-----AEMLC-----STLKKQK-KFLERODETKQAREEAAH 157

Db 1626 NKEELKTLNORLAEMLCOREPACGCTSEKWEQENASLKEELDHKKVOTSLVSSLEAELS 1685
Qy 158 RLKCKMTMEIOELLLOSORSEVEEMTR--DMVGOSAVROALAVYCVSLKKEVE----- 209
Db 1686 RIKLQTHMEQENLLLEDELRKQLHRCPDLSLQOKMSSVSLYNKLEKKEVLSLEEL 1745
Qy 210 -----NKEAKATGELADRLKDLVSSRSKLTNTLELDAQLELR 251
Db 1746 KSCADKLAESSLLEHRTATKKEQOTAMEQESLSQSLAVSQAVQDELDVLOVNVNLQMA 1805
Qy 252 SAQKDLO-----SADQETSLRKK-----SDPPGNEPASAETIVS----- 289
Db 1806 EIESDLOVTRQEKRAVQEWMSLHRQLNADIKDMVSEETAP-HLSGLRGQORRLSMDKLD 1864
Qy 290 RLVEESPAPYEMMNRHLQHPPEFGDEIDLNTT-----FDVTPPT--QTSSQHCLEPKL 341
Db 1865 HLMNEEPOLLOESKRKLQTVVONTQADTHSRKRVKQLESLLPTKHOKOLNQPCTVKS- 1933
Qy 342 CLERARSPMONVLTKKVKVSKPESQSLGQRCVGELEDELAGAPPLFIRNAVLGQR--Q 399
Db 1924 -TEQEKTLKRECEQSQKESQPS-----RKYGQMSGLERGLTHLENEGKTKKQMQ 1975
Qy 400 PNRTAESRSST 411
Db 1976 PLRSTVTRSPSS 1987

RESULT 26
A27224
myosin heavy chain II - Acanthamoeba castellanii
N:Contains: myosin ATPase (EC 3.6.1.32)
C:Species: Acanthamoeba castellanii
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C:Accession: A27224
R:Hammer II, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
J. Cell Biol. 105, 913-925, 1987
A:Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle my
A:Reference number: A27224; MUID:87308395
A:Accession: A27224
A:Molecule type: DNA
A:Residues: 1-1509 <HAM>
A:Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:95585; PIDN:CAA68663
C:Genetics:
A:Introns: 69/3; 119/3; 181/2
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide
F:92-775/Domain: myosin motor domain homology <MMOT>
F:182-189/Region: nucleotide-binding motif A (P-loop)
F:544-576/Region: actin binding #status predicted
F:660-682/Region: actin binding #status predicted
F:848-1227/Domain: coiled coil #status predicted <COI>
F:1228-1247/Domain: hinge <HIN>
F:1448-1482/Domain: coiled coil #status predicted <CO2>
F:1483-1509/Domain: carboxyl-terminal <CBT>
F:133/Modified site: N6; N6-trimethyllysine (Lys) #status predicted
F:188/Binding site: ATP (Lys) #status predicted

Query Match 7.4%; Score 176.5; DB 1; Length 1509;
Best Local Similarity 24.5%; Pred. No. 0.13;
Matches 81; Conservative 63; Mismatches 113; Indels 73; Gaps 15;
Qy 66 LAOEENVLDAEFLKNELDSVKAQLSQKDRKRSQAIIIDRLRLTERNA-----TVESL 121
Db 888 LAEE-----DADKLEKDLALKLTLDLEGRAD-----LEEDNALOKKAVGL 931
Qy 122 QNALNKAEMLSLTKQMKFLEORODETKQAREBAHRLCKMKMTMEIOELLLOSORSEVE 181
Db 932 EEELOEERSASNDILEQKRKLEAEKGLAKASLEEBER--NRKALQEKATVESERNLQ 988
Qy 182 EMIRDMVGOSAVROALAVYCVSLKKEVENL-KEARKATGELAD--RLKKDLVSSRSKLT 238
Db 989 DKYEDEAAAH-----SLKKKEEDLSRELRKTDALADAEINISETL---RSKLN 1035

Qy 239 -----LNTLEDO---AKLELSAOKDLSADOETSLRKKSDPPGNEPASAETIV 288
Db 1036 TERGADVRYNELDDVATKTLQLEKTKSL--EELQOTRAOLEEKSGEAASSRAKOL 1092
Qy 289 SRLVESAPYEMMNRHLQHPPEFGDEIDLNTTVDVNTPTQTSQSHCLPKLCLERARS 348
Db 1093 GQQLDARSEVDSLKSLTS-----AAKSLKTVAKQONNDLDEQ-----LEDERT 1136
Qy 349 PMONVLKVVH-----KVKPESQL-SLGGQR 373
Db 1137 VRANVDKQKALEKAKLTLEDVQVYALDQK 1166

RESULT 27
T16270
hypothetical protein F35D11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16270
R:Fullon, B.
Submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F35D11.
A:Reference number: Z18487
A:Accession: T16270
A:Molecule type: DNA
A:Residues: 1-1827 <FUL>
A:Cross-references: EMBL:029381; NID:9868214; PID:9868224; PIDN:AAA68757.1; CESP:F35D
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F35D11.11
A:Introns: 76/2; 131/3; 159/3; 185/3; 221/3; 253/3; 320/1; 869/3; 1133/3; 1205/2; 125

Query Match 7.4%; Score 176.5; DB 2; Length 1827;
Best Local Similarity 25.3%; Pred. No. 0.16;
Matches 61; Conservative 63; Mismatches 82; Indels 35; Gaps 9;

Qy 52 QVQKKT-----IINKLFPLDAOEENVD-----AEFLKNELDSVKAQLSQKDRKRD 99
Db 657 QVNERTRQISEANKKYDDAARKNDALLLEDVATWQEKYEOLKMELEEMNRGQEKEREED 716
Qy 100 SQAIIDTLR-----DTLEERNATVESIQNALKKAEMLSLTKKM-KFLEORODETKQ 151
Db 717 LRALLDRLRGFNDKLTNELKQGVTVDSLNEI-----SLKEQLKSEKEREKEELR 769
Qy 152 AREBAHRLCKMKMTMEIOEL-LLOSORSEVEEMIRDMVGOSAVROALAVYCVSLKKEYEN 210
Db 770 MEELQKNEAMKREYEVKQLQAKEDQGVENPQKEC---EARNNELTKHIMLEMEHDQ 826
Qy 211 LKEARKATGELADRLKDLVSSRSKLTNTLELDAQLELSAOKDLSADQF-ITSRLK 269
Db 827 LKVQHLHTEEEVERLKEKM--RKLEKLNQNDGDRAEWSENRNRLESSKNEAVTELQ 883
Qy 270 K 270
Db 884 R 884
RESULT 28
B44972
paramyosin - nematode (Onchocerca volvulus) (fragments)
C:Species: Onchocerca volvulus
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 02-Jul-1998
C:Accession: B44972
R:Limberger, R.J.; McReynolds, L.A.
Mol. Biochem. Parasitol. 38, 271-280, 1990
A:Title: Filarial paramyosin: cDNA sequences from Dirofilaria immitis and Onchocerca
A:Reference number: A44972; MUID:90220759
A:Accession: B44972
A:Status: preliminary
A:Molecule type: mRNA

Db 406 YENEDIKRLAEKERLS-----SRITIIKAKL--PGIREVEK----- 442

Qy 332 GSOHCLPKLCLERASPMONVKKVHKVSKRESOLSGORCVGEDE---ELAGAPFL 388

Db 443 -----LREK--LEKKALSNVENKISSIQRRKVEELEKKSELOKVSSELSERE 495

Qy 389 FIRNAVLCQKQPNRTTASRSSTDVVRIGFDGRTKFIQPRDTTIIIPVYSKRAKS 447

Db 496 LIKAEQSEVHVNRVAEELK-----RSGISGIYG-----TILELIRVDEWYS 538

RESULT 33

F96673

hypothetical protein F13011.30 [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F96673

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizart, L.

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F96673

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1313 <STO>

A:Cross-references: GB:AE005173; NID:95042434; PIDN:AAD38273.1; GSPDB:GN00141

C:Genetics:

A:Gene: F13011.30

A:Map position: 1

Query Match 7.3%; Score 175; DB 2; Length 1313;

Best Local Similarity 21.9%; Pred. No. 0.13;

Matches 100; Conservative 81; Mismatches 126; Indels 150; Gaps 20;

Qy 67 AOEENVID-----AEFLKELDSYKAOL--SOKDREKDSQAIIDTLRLTEERNATVES 120

Db 182 AEEATKIAEIAEKAELIASLGLKALSGKEKEALEGNEIYSKIL-----SEIEL 234

Qy 121 LQNLNKAEMICSTLKKQMKFLQRODETKQAR-----FEA 156

Db 235 LRGELKRVSILESSLKEQGLVEQLKVDLEAKMAESCSTNSSVEEMKNKVELEKEVEES 294

Qy 157 HRLCK-----MKTW-----EOIELL--LOSORSEVEEMTRDM 187

Db 295 NRSSSASSESMYKQALAEINHYLHETKSDNAOKETIELLETTIEQKRTDELEYGHV 354

Qy 188 GVGSAAVEQLAVYCVSLKREYE-----NLKEARKATGELAD----- 223

Db 355 CIAKEASKLENTVESIKSELEISQEKTRALDNKATSNITQNLQDRTLESTLEERCK 414

Qy 224 -----RLKDLVSSRSKLTLTLEIDQAKLEKSAQKDLQADQETSLCKRSSDPGNLE 279

Db 415 VEEKRSKDKMDESLTALQEAESTESSEKATLLVCQEEIKNCESOVDSIKLASKE----- 468

Qy 280 PASATNETVSRVLESPAPVEMMNPRLHQPFGDEID-LNTTPD--VNTPTQTSQSGHC 336

Db 469 -----TNEKYEMLEDA-----RNEIDSLKSTVSIQNEFENSRAGWEO- 507

Qy 337 LPKKL-----CLERAR-----SPMONVKKRVHK--VSKPESQSLSGQRCVGE--- 377

Db 508 --KELHLMGCVKKSSEENSSQGEVSRVYNLTKSEEDACARKDEEASLKNNLKVAAGEV 565

Qy 378 --LDEEL--AGAPFLFIRNAVLCQKQPNRTTASRS 409

Db 566 KYLOETLGEAKAESMKLKESLDKREEDLKNTVAEISS 602

RESULT 34

I52300

giantin - human

N:Alternate names: gcp372

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Aug-1999

C:Accession: I52300

R:Schda, M.; Misumi, Y.; Fujiwara, T.; Nishioke, M.; Ikehara, Y.

Biochem. Biophys. Res. Commun. 205, 1399-1408, 1994

A:Title: Molecular cloning and sequence analysis of a human 372-kDa protein localized

A:Reference number: I52300; MUID:95100974

A:Accession: I52300

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3225 <RES>

A:Cross-references: GB:I25542; NID:9662389; PIDN:BA05025.1; PID:9808869

C:Superfamily: giantin

Query Match 7.3%; Score 174.5; DB 2; Length 3225;

Best Local Similarity 21.1%; Pred. No. 0.39;

Matches 115; Conservative 88; Mismatches 174; Indels 169; Gaps 20;

Qy 30 HLOCLIQMFE-----TAPSRTPCPCRIQYGGKTIINKLPFDLQAEENVLDA--- 76

Db 686 NLNOLIEEFKKNADNNSAFTALSEERDQLSQYKELSMWTELRAQYKQLEMLAEERQ 745

Qy 77 -----ETLKNELDSYKAOL--SOKDREKDSQAI 103

Db 746 RRLDYESQTAHNDLITQIHSLSIEAKSKDVKIEVLQNELDVQLOFSEOSTLRSLSQ 805

Qy 104 IDTLR-DTLE--ER-----NATVESIQNALNKAE-----ICSTLKKQKKFLQRODET 149

Db 806 LQNKSEVLBGAEKRVRIHSKVEELSQLSOKELITKMDQLLEKRDVETTLQOTLEEK 865

Qy 150 K-----QAREAHRLKCKMKTW--EOIELLLOSORSEVEEMI RDMGV---- 189

Db 866 DQQVTEISFMTKEMQVNLNEKFSLGVEITKLRQMLNLSRAEAKKEQYEDNEVSSGL 925

Qy 190 -----GQSAVEQLAVYCVSLKREYENLKA-----RKATGELADRLKDLVSS 232

Db 926 KQNYDEMSPAGQISKEELQHEFDLKKENQRKRLQALINRKELQIRVSRLEEEELANL 985

Qy 233 RSKLKT-----LNTELDQAKLEIRSNQKD 256

Db 986 KDESKEEIPUSETGERGEVEEDKENKEYSEKCVTSKCOEIEIYKQITSEKEVELQHTRKD 1045

Qy 257 LQ--SADQETSLRKKSDPPGNLEPASATNETVSRVLESPAPVEMMNPRLHQPFGD 313

Db 1046 LEKTLAEBEQPALVKNQMNQ--TLQDKTNOIDLQAEISENQAIITKLTSTNDASDGD 1102

Qy 314 EIDLNTTFDVNTPTQTSQSGOHLR--KKLCERASPMONVKK-----VHKVS 361

Db 1103 SVALVRETVVISPCC--TGSSEHMKPELEKILALEKREKQLOKKLQALRSRAKILK 1161

Qy 362 KPESQL--SLGGQ-----RCVGELE-----ELAGAPFLFIRNAVLCQKQPNRTTA 405

Db 1162 EKERHLEELKQKQDDVNRLOEQDPEOSKENENIGDROLQLOIJOVERSIDG-KLPSTDOQ 1220

Qy 406 ESRNST 411

Db 1221 ESCSST 1226

RESULT 35

A56539

giantin - human

N:Alternate names: macroglobin

C:Species: Homo sapiens (man)

C:Date: 19-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 10-Dec-1999

C:Accession: A56539; S37536

R;Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.; Griffiths, G.; Renz, M.
Mol. Cell. Biol. 14, 2564-2576, 1994
A:Title: Molecular genetic analyses of a 376-kilodalton Golgi complex membrane protein
A:Reference number: A56539; MUID:94107728
A:Accession: A56539
A:Molecule type: mRNA
A:Residues: 1-3259 <SEE>
A:Cross-references: EMBL:X75304; NID:9405714; PIDN:CA53052.1; PID:9405715
C:Genetics:
A:Gene: GDB:GOLGB1; GCP:GCP371
A:Cross-references: GDB:454958
A:Map position: 3q13.31-3q13.31
C:Superfamily: giantin
C:Keywords: coiled coil; Golgi apparatus; transmembrane protein
F:3338-3254/Domain: transmembrane #status predicted <TM>

Query Match 7.3%; Score 174.5; DB 1; Length 3259;
Best Local Similarity 21.1%; Pred. No. 0.39;
Matches 115; Conservative 88; Mismatches 174; Indels 169; Gaps 20;

QY 30 HLOCLIMFE-----TAPSTPCQCRIOYGGKTIINKLFEDLAQEEENLDA--- 76
DB 720 NLNQLIEFKKNADNNSAFTALSEERDQLSYKELSMVETLRAQYKOLEMNLAEERQ 779
QY 77 -----EFLKNELDSVKAQLSOKDKREKRSQAI 103
DB 780 RLIDYESOTAHNDLTLTQIHSLTEAKSKDYKITEVLONELDDVLOQSEGTILRSLSQ 839
QY 104 IDTLR-DTLE--ER-----NATESLONLANKAEM-----LCSTLKKQMKLEBODET 149
DB 840 LONKESELEGAERHVRHISSEVELSOLSQELEITRMQDLLEKKRDVETLQOTIEK 899
QY 150 K-----QAREAHRLKCKMKTM-BOIELLOSQSEVEEMRDGCV---- 189
DB 900 DQVTEISFSTKEMVOLNEKEFSLGVEIKTLKEQLNLHRAEBAKKEQVEDNEVSSGL 959
QY 190 -----GQSAVEDLAVYCVSLKKEYEENLKEA-----RKATGELADLKKDLVSS 232
DB 960 KQNDENSPAGQISKEELQHFEDLKKENBQRKKLQALINKRELLQVRSLEBELANL 1019
QY 233 RSKLKT-----LWTELDQAKLELRSQKD 256
DB 1020 KDECKEILPSETERGEVEEDKENKEYSEKCVTSKCEIEIYLKQITSEKEVELOHTRKD 1079
QY 257 LQ-----SADQETSLRKSSDDPGNLERASATNEVSRVESPAPVEMMRLQPPGCD 313
DB 1080 LEKLAEEQFOALVKQWNO---TLQDKTQIDLLQAEISENOALIKLITSNTDASGD 1136
QY 314 EIDNTTFDVNTPTQTSGSOHCLP---KILCLERARSPQWNLKK-----VHKVS 361
DB 1137 SVALLVKEVIVISPPC-TGSSSHMKRPELEKTLAEKEKEQLOKLOELVTSRKAILKKAQ 1195
QY 362 KPESOL-SLGGQ-----RCVGELE-----ELAGAPLFIINAVALQOKPNRTTA 405
DB 1196 EKENHLEELKQKQDDYNRLOEQFDEQSKENENIGDQLRQIQIQRRESID-KLPSTFQD 1254
QY 406 ESRSSST 411
DB 1255 ESCSST 1260

RESULT 36
S00084
myosin heavy chain, fast skeletal muscle - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: S00084; S14807
R;Mada, K.; Sczakiel, G.; Wittlinghofer, A.
Eur. J. Biochem. 167, 97-102, 1987
A:Title: Characterization of cDNA coding for the complete light meromyosin portion of a
A:Reference number: S00084; MUID:87304245
A:Accession: S00084

A:Molecule type: mRNA
A:Residues: 1-676 <MAE>
A:Cross-references: EMBL:X05958; NID:91622; PIDN:CA29391.1; PID:91364242
A>Note: the sequence from Fig. 5 is inconsistent with that from Fig. 3 in having 561-
R;Mada, K.; Roesch, A.; Mada, Y.; Kaldtzer, H.R.; Wittlinghofer, A.
FEBS Lett. 281, 23-26, 1991
A:Title: Rabbit skeletal muscle myosin. Unfolded carboxyl-terminus and its role in mo
A:Reference number: S14807; MUID:91200294
A:Accession: S14807
A>Status: preliminary
A:Molecule type: protein
A:Residues: 668-676 <MA2>
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle
F:21-676/Domain: light meromyosin <LM>

Query Match 7.3%; Score 174; DB 2; Length 676;
Best Local Similarity 20.8%; Pred. No. 0.069;
Matches 80; Conservative 81; Mismatches 157; Indels 66; Gaps 13;

QY 68 QEENNVDAEFLKELDSVA-----QLSQND-----REKRSQAI---IDTLRD 109
DB 3 KEEEH---ORLINLSAQRARLHTESGERSQIDEKDAWVSQLSRGQAFTQIQIEGLR 58
QY 110 TLEERNATVESLONLANKAEMLCSTLKKQMKFLBODETFOAREEAAH-----RLCKM 163
DB 59 QLEETRAKSAHALALOSSRRDCDLREQYEEDEKAELQARMSKANSEYQRTGCET 118
QY 164 KTMBOIELLOSQSEVEEMIRDMGVQSAVEQALAVYCVSLKKEYEENLKEARKATGELAD 223
DB 119 DAIO RTE-ELEBAKKLQARLOD---AEHVEAVNSKCAISLEKTKORLO--NEAEDLMID 172
QY 224 RLKRDVSSRKLTLMTE-----LQAKLELSAQKLDLSAQOETSLRKSSDDP 274
DB 173 VERSNATCARDKQRNFQVLAEMKHYETQALASQESKRSLSSTEFVKYNAVEES 232
QY 275 PGNLEPASATNETVSRVESPAPVEMMRLHQ-PPFGDEIDNTTFDVNTPTQTSGS 333
DB 233 LDHETLKKREKNLQOETSDLTEDIASAKIHILEVKKQID----- 275
QY 334 QHCLPRKLCLEERARSPQWNLKVKVSKPESQLSGORCVGLDELAGAPLFIINA 393
DB 276 QEKSELQALAEAGCSLEHGEKILRIQLLELVKSEIDRIAKKDEI-----DQLKRNH 331
QY 394 V-LGQKQPNRTTASRSSTDVRI 416
DB 332 LRVESMSTLDLAEIRSRNDALRI 355

RESULT 37
B55094
chromosomal protein XCAP-E - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
C:Accession: B55094
R;Hirano, T.; Mitchison, T.J.
Cell 79, 449-458, 1994
A:Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensa
A:Reference number: A55094; MUID:95042742
A:Accession: B55094
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1203 <HIR>
A:Cross-references: GB:U13674; NID:9563813; PIDN:AAA64680.1; PID:9563814
C:Superfamily: chromosome segregation protein SMCI
C:Keywords: chromosomal protein; DNA condensation; heterodimer

Query Match 7.3%; Score 173.5; DB 2; Length 1203;
Best Local Similarity 21.9%; Pred. No. 0.14;
Matches 73; Conservative 69; Mismatches 135; Indels 57; Gaps 11;

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0Y 77 EFLNKLDSVVAQKSDKDREKRDQSOAILPTLROTTERNATVSLONALKNMCJSTLK 136
Db 721 EMKEEAEILOTTKQOQSYHKQOEE--LDJSLKOTIESEETLNTXEVOKAEKRYALE 778
0Y 137 KOMFLE-ORODETKQARE-----EABRLCKCMKJTEQJELLQSORSEVEEMIRD 186
Db 779 HKMKNNAERERRELKEAQOKLDTAKKAKADSNNKKMEKQOEVALVY-----ELEBLAKE 833
0Y 187 MGVQSAVEQLAVYCVSLKEYEYLNKERRATGELADRLKLDVSSRSKJTLNTELDQA 246
Db 834 Q-----TYYKQOIEYDEAMKAYQOQDSMASEVSKNKEAVKKAQOELARQ 879
0Y 247 KLEIRSAQKDLQSDQOETSLSRKSDPPCNLEPASTNETTYSRLVESPAPY-EMMN- 304
Db 880 KEIIMGHDKELIKTSSEAGRLNRENTLOJIKELIHINISIKHKKDSADAAKAVAKMLNDY 939
0Y 305 ---RLHQPPDEDELDTTVDVMTPTQJSGSQ-HCLPKL-----CLERAK 347
Db 940 EMIASEKHLSG---QANTAVDFKTNPNKEGQRLHKLOEKREKLGNNVMMRAMMLTQAE 996
0Y 348 SPMONVLKRYKVKSPESQSLSGQRCVGLDEE 381
Db 997 ERYNDLKKRKYIENDKSKT---LTTIEELDOK 1026

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QY 55 KTTINKLPFDLAQEEENVLADEFKLNELDSVKAQLSQKDRKDSQAIIIDTLRDTLEER 114
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1269 QQRRLNDL---TQRRARLQREAGEYSRQDDEKDALVSQLSRSQAOSTQOIELKHQEE 1325
QY 115 NATVESIQNALNKAEMLCSLTKOMKFLERQDQETKQAREBAHRLCKMKTMOIEILLQ 174
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1326 TKAKNALAHALOSSRHCCDLRLREQYEEBQDKAELQALSKANSEVQOMRTKYETDAIQ 1385
QY 175 SQRSEVEE---MIRMGVGSASAEQDLAVYCVSLKKEYLENK-----EARKATGE 220
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1386 TE--ELBEAKKKAQROEAEEHVEAVNAKCALEKTKQRLQNEVEDLMIDVESNACA 1443
QY 221 LADRLKK--DLVSSRSKLTNTLTDQAKLELSAQKDLSAQOELTSLRKKSDPPGNL 278
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1444 ALDKQKNFQKVLSEMKQK-----YEETQALEASQKESRSLSTELFKVKNVYEESIDL 1498
QY 279 EPASATNETVSRVLFESPAPVEEMNPRLHQPPGDEIDLNTTFDVNTPPTQSGSQHCLP 338
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1499 ETLRREKKNLQOETISDLTEQIAEGKQIHE-----LEKIKKQVEQKE 1542
QY 339 KKLCLERARSPMGNVLKVKYKSPESQSLGRCYGELEDELAGAFPLFIRNAVIGOK 398
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1543 IQAALBEAEASLHEBEGKILRIQLELNQVKSVDKRTAEKDE-----IDQL 1589
QY 399 QPNRT-----TAESRSSTDVRI 416
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1590 KRHNTRVETMOSTLDAEIRSRNDALRV 1617

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RESULT 40
T51505
hypothetical protein F5E19_70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51505
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Men
submitted to the Protein Sequence Database, August 2000
A:Reference number: 225394
A:Accession: T51505
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-853 <SAT>
A:Cross-references: EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 6/2; 79/3
A>Note: F5E19_70

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Query Match 7.2%; Score 171.5; DB 2; Length 853;
Best Local Similarity 19.7%; Pred. No. 0.12;
Matches 82; Conservative 92; Mismatches 148; Indels 95; Gaps 14;

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QY 66 LAQEEENVLADEFKLNELDSVKAQLSQKDRKDSQAIIIDTLRDTLEERNATVESIQNAL 125
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 382 VAKQKE---DLEVSQRLGSEVEEVSKNEKEVEKLKSELETVK---EKNRALKKEDAT 435
QY 126 NKAEMLCSTLKQMKFLE---QRODETQKARE-----EAHRLCKMKPT----- 165
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 436 SRVQRLSEESKSLIDLESSEKSEKESKAMESLASALHEVSSGRELKELKLSQGDHEY 495
QY 166 ---MEQIELLQSORSEVEEMI---RDMGVGSASAEQDLAVYCVSLKKEYLENKEAR--- 215
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 496 ETQIDDKLVKATNEKENMLDEARHEIDVLVSVEQTKKHFESSKKDWE-MKEANLVN 554
QY 216 -----KATGELADRLKKDLVSSRSKLTNTLNTL-----LDQ 245
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 555 YVKKMEEDVASMGEKMRNLNLKRTKEEADAAKKKAQTKDSLKEVEBEELVYIQETLGE 614
QY 246 AKLELRSAGQDLQSDQETSLRKKSDPPGNLEPASATNETVSRVLFESPAPVEEMNPR 305
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 615 AKAESMKLKENLLDKETEFQNVIHENEDLKAKEVDLSLKKIEELSKLLEEA-----ILAKK 669
QY 306 LHQPPGDEIDLNTTFDVNTPPTQSGSQHCLPK--KLCLERARSPMGNVLKVKHY--S 361
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 670 QPEBENGELSEKDYDL-----LPRVVEFSSNGHRSVEEKSAAVETLDHE 716
QY 362 KPSQSLGRCYGELEDELAGAFPLFIRNAVIGOKQPNRTTAESRSSTDVRI 418
   :|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 717 PQEQIISNGNSNGMGEKEVNG-----KPEVTEKKEKKESQDDDKDSVEVIF 767

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Search completed: September 4, 2002, 16:12:55
Job time: 3239 sec

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